

WO 03/072014

PCT/US02/16877

1441

CGTGATGCCTGCACCTATGCCACAGCCCTCAATGTAGCCAGCCTGAGTGTGGAGC
GCTAC

481 R D A C T Y A T A L N V A S L S V E R Y

5

1501

TTGGCCATCTGCCATCCCTTCAAGGCCAAGACCCTCATGTCCCGCAGCCGCACCA
AGAAA

501 L A I C H P F K A K T L M S R S R T K K

10

1561

TTCATCAGTGCCATATGGCTAGCTTCGGCGCTGCTGGCTATACCCATGCTTTTCAC
CATG

521 F I S A I W L A S A L L A I P M L F T M

15

1621

GGCCTGCAGAACCGCAGTGGTGACGGCACGCACCCTGGCGGCCTGGTGTGCACAC
CCATT

541 G L Q N R S G D G T H P G G L V C T P I

20

1681

GTGGACACAGCCACTGTCAAGGTCGTCATCCAGGTAAACACCTTCATGTCCTTCCT
GTTT

561 V D T A T V K V V I Q V N T F M S F L F

25

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PCT/US02/16877

1741

CCCATGTTGGTCATCTCCATCCTAAACACCGTGATTGCCAACAACTGACAGTCAT
GGTG

581 P M L V I S I L N T V I A N K L T V M V

5

1801

CACCAGGCCGCCGAGCAGGGCCGAGTGTGCACCGTGGGCACACACAACGGTTTAG
AGCAC

601 H Q A A E Q G R V C T V G T H N G L E H

10

1861

AGCACGTTCAACATGACCATCGAGCCGGGTCGTGTCCAGGCCCTGCGCCACGGAG
TCCTC

621 S T F N M T I E P G R V Q A L R H G V L

15

1921

GTCTTACGTGCTGTGGTCATTGCCTTTGTGGTCTGCTGGCTGCCCTACCACGTGCG
ACGC

641 V L R A V V I A F V V C W L P Y H V R R

20

1981

CTGATGTTCTGCTATATCTCGGATGAACAGTGGACTACGTTCTCTTCGATTTCTA
CCAC

661 L M F C Y I S D E Q W T T F L F D F Y H

25

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PCT/US02/16877

2041

TATTTCTACATGCTAACCAACGCTCTCTTCTACGTCAGCTCCGCCATCAATCCCAT
CCTC

681 Y F Y M L T N A L F Y V S S A I N P I L

5

2101

TACAACCTGGTCTCCGCCAACTTCCGCCAGGTCTTTCTGTCCACGCTGGCCTGCCT
TTGT

701 Y N L V S A N F R Q V F L S T L A C L C

10

2161

CCTGGGTGGCGCCACCGCCGAAAGAAGAGGCCAACGTTCTCCAGGAAGCCCAACA
GCATG

721 P G W R H R R K K R P T F S R K P N S M

15

NotI +2 TrxA

2221

TCCAGCAACCATGCCTTTTCCACCAGCGCCACCCGGGAGACCCTGTACgcgggccgcaA
GC

20

741 S S N H A F S T S A T R E T L Y A A A S

2281

GATAAAATTATTACCTGACTGACGACAGTTTTGACACGGATGTACTCAAAGCGG
ACGGG

25

761 D K I I H L T D D S F D T D V L K A D G

WO 03/072014

PCT/US02/16877

2341

GCGATCCTCGTCGATTTCTGGGCAGAGTGGTGCGGTCCGTGCAAAATGATCGCCC
CGATT

5 781 A I L V D F W A E W C G P C K M I A P I

2401

CTGGATGAAATCGCTGACGAATATCAGGGCAAACCTGACCGTTGCAAAACTGAACA
TCGAT

10 801 L D E I A D E Y Q G K L T V A K L N I D

2461

CAAAACCCTGGCACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTGC
TGTTT

15 821 Q N P G T A P K Y G I R G I P T L L L F

2521

AAAAACGGTGAAGTGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTGA
AAGAG

20 841 K N G E V A A T K V G A L S K G Q L K E

NotI +2 Flag

stop

2581

TTCCTCGACGCTAACCTGGCGgcggccgcaGATTATAAAGATGACGATGACAAATAAT

25 AA

PCT/US02/16877

861 F L D A N L A A A A D Y K D D D D K * *

KpnI

2641 GGTACC

5

SEQ ID NO.: 170

10 MalE (1-28) Factor Xa NTR (43-424) TrxA (2-109) FLAG

SalI +1 MalE leader (1-28)

1

gtcgacATGAAATAAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACG
15 ATGATGTTT

1 M K I K T G A R I L A L S A L T T M M F

Factor Xa +43 NTR

61

20 TCCGCCTCGGCTCTCGCCAAAATCATCGAAGCCCGCACCTCGGAATCCGACACGG
CAGGG

21 S A S A L A K I I E A R T S E S D T A G

WO 03/072014

PCT/US02/16877

121

CCCAACAGCGACCTGGACGTGAACACTGACATTTATTCCAAGGTGCTGGTGACTG
CTATA

41 P N S D L D V N T D I Y S K V L V T A I

5

181

TACCTGGCACTCTTCGTGGTGGGCACTGTGGGCAACTCCGTGACAGCCTTCACTCT
AGCG

61 Y L A L F V V G T V G N S V T A F T L A

10

241

CGGAAGAAGTCACTGCAGAGCCTGCAGAGCACTGTGCATTACCACCTGGGCAGCC
TGGCA

81 R K K S L Q S L Q S T V H Y H L G S L A

15

301

CTGTCCGACCTGCTTATCCTTCTGCTGGCCATGCCCCTGGAGCTATACAACTTCAT
CTGG

101 L S D L L I L L L A M P V E L Y N F I W

20

361

GTACACCATCCCTGGGCCTTTGGGGACGCTGGCTGCCGTGGCTACTATTCCTGCG
TGAT

121 V H H P W A F G D A G C R G Y Y F L R D

25

PCT/US02/16877

GCCTGCACCTATGCCACAGCCCTCAATGTAGCCAGCCTGAGTGTGGAGCGCTACT
TGGCC

5

ATCTGCCATCCCTTCAAGGCCAAGACCCTCATGTCCCGCAGCCGCACCAAGAAAT
TCATC

10

AGTGCCATATGGCTAGCTTCGGCGCTGCTGGCTATACCCATGCTTTTCACCATGGG
CCTG

15

CAGAACCGCAGTGGTGACGGCACGCACCCTGGCGGCCTGGTGTGCACACCCATTG
TGGAC

20

ACAGCCACTGTCAAGGTCGTCATCCAGGTTAACACCTTCATGTCCTTCCTGTTTCC
CATG

25

WO 03/072014

PCT/US02/16877

721

TTGGTCATCTCCATCCTAAACACCGTGATTGCCAACAACTGACAGTCATGGTGCA
CCAG

241 L V I S I L N T V I A N K L T V M V H Q

5

781

GCCGCCGAGCAGGGCCGAGTGTGCACCGTGGGCACACAACGGTTTAGAGCACA
GCACG

261 A A E Q G R V C T V G T H N G L E H S T

10

841

TTCAACATGACCATCGAGCCGGGTCGTGTCCAGGCCCTGCGCCACGGAGTCCTCG
TCTTA

281 F N M T I E P G R V Q A L R H G V L V L

15

901

CGTGCTGTGGTCATTGCCTTTGTGGTCTGCTGGCTGCCCTACCACGTGCGACGCCT
GATG

301 R A V V I A F V V C W L P Y H V R R L M

20

961

TTCTGCTATATCTCGGATGAACAGTGGACTACGTTCCCTCTTCGATTTCTACCACTA
TTTC

321 F C Y I S D E Q W T T F L F D F Y H Y F

25

PCT/US02/16877

TACATGCTAACCAACGCTCTCTTCTACGTCAGCTCCGCCATCAATCCCATCCTCTA
CAAC

341 Y M L T N A L F Y V S S A I N P I L Y N

5

CTGGTCTCCGCCAACTTCGCCAGGTCTTTCTGTCCACGCTGGCCTGCCTTTGTCC
TGGG

361 L V S A N F R Q V F L S T L A C L C P G

10

TGGCGCCACCGCCGAAAGAAGAGGCCAACGTTCTCCAGGAAGCCCAACAGCATGT
CCAGC

381 W R H R R K K R P T F S R K P N S M S S

15

NotI +2 TrxA

AACCATGCCTTTTCCACCAGCGCCACCCGGGAGACCCTGTACgggcgcaAGCGATA
AA

20

401 N H A F S T S A T R E T L Y A A A S D K

ATTATTACCTGACTGACGACAGTTTTGACACGGATGTACTCAAAGCGGACGGGG
CGATC

25

421 I I H L T D D S F D T D V L K A D G A I

WO 03/072014

PCT/US02/16877

1321

CTCGTCGATTTCTGGGCAGAGTGGTGCGGTCCGTGCAAAATGATCGCCCCGATTCT
GGAT

5 441 L V D F W A E W C G P C K M I A P I L D

1381

GAAATCGCTGACGAATATCAGGGCAAACCTGACCGTTGCAAAACTGAACATCGATC
AAAAC

10 461 E I A D E Y Q G K L T V A K L N I D Q N

1441

CCTGGCACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTGCTGTTCAA
AAAC

15 481 P G T A P K Y G I R G I P T L L L F K N

1501

GGTGAAGTGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTGAAAGAGT
TCCTC

20 501 G E V A A T K V G A L S K G Q L K E F L

NotI Flag stop KpnI

1561

GACGCTAACCTGGCAgcggccgcaGATTATAAAGATGACGATGACAAATAATAAGGTA
25 CC

WO 03/072014

PCT/US02/16877

521 D A N L A A A A D Y K D D D D K

5 SEQ ID NO.: 188

Human 2AR GS1 chimeric fusion

SalI +1 B2AR

10 1 GTCGACATGG GGCAACCCGG GAACGGCAGC GCCTTCTTGC
 TGGCACCCAA TGGAAGCCAT

 61 GCGCCGGACC ACGACGTCAC GCAGCAAAGG GACGAGGTGT
 GGGTGGTGGG CATGGGCATC

15 121 GTCATGTCTC TCATCGTCCT GGCCATCGTG TTTGGCAATG
 TGCTGGTCAT CACAGCCATT

 181 GCCAAGTTCG AGCGTCTGCA GACGGTCACC AACTACTTCA
 TCACTTCACT GGCCTGTGCT

 241 GATCTGGTCA TGGGCCTAGC AGTGGTGCCC TTTGGGGCCG
20 CCCATATTCT TATGAAAATG

 301 TGGACTTTTG GCAACTTCTG GTGCGAGTTT TGGACTTCCA
 TTGATGTGCT GTGCGTCACG

 361 GCCAGCATTG AGACCCTGTG CGTGATCGCA GTGGATCGCT
 ACTTTGCCAT TACTTCACCT

WO 03/072014

PCT/US02/16877

421 TTCAAGTACC AGAGCCTGCT GACCAAGAAT AAGGCCCCGGG
TGATCATTCT GATGGTGTGG

481 ATTGTGTCAG GCCTTAYCTC CTTCTTGCCC ATTCAGATGC
ACTGGTACAG GGCCACCCAC

5 541 CAGGAAGCCA TCAACTGCTA TGCCAATGAG ACCTGCTGTG
ACTTCTTCAC GAACCAAGCC

601 TATGCCATTG CCTCTTCCAT CGTGTCTTC TACGTTCCCC
TGGTGATCAT GGTCTTCGTC

661 TACTCCAGGG TCTTTCAGGA GGCCAAAAGG CAGCTCCAGA
10 AGATTGACAA ATCTGAGGGC

721 CGCTTCCATG TCCAGAACCT TAGCCAGGTG GAGCAGGATG
GGCGGACGGG GCATGGACTC

781 CGCAGATCTT CCAAGTTCTG CTTGAAGGAG CACAAAGCCC
TCAAGACGTT AGGCATCATC

15 841 ATGGGCACTT TCACCCTCTG CTGGCTGCCC TTCTTCATCG
TTAACATTGT GCATGTGATC

901 CAGGATAACC TCATCCGTAA GGAAGTTTAC ATCCTCCTAA
ATTGGATAGG CTATGTCAAT

961 TCTGGTTTCA ATCCCCTTAT CTACTGCCGG AGCCCAGATT
20 TCAGGATTGC CTTCCAGGAG

1021 CTTCTGTGCC TGC GCAGGTC TTCTTTGAAG GCCTATGGCA
ATGGCTACTC CAGCAACGGC

1081 AACACAGGGG AGCAGAGTGG ATATCACGTG GAACAGGAGA
AAGAAAATAA ACTGCTGTGT

1141 GAAGACCTCC CAGGCACGGA AGACTTTGTG GGCCATCAAG
25 GTACTGTGCC TAGCGATAAC

WO 03/072014

PCT/US02/16877

Last B2AR Linker

sequence

1201 ATTGATTCAC AAGGGAGGAA TTGTAGTACA AATGACTCAC
5 TGCTAGAGCG TGGCCAGACG

PstI XhoI +2 GS1 alpha

1261 GTCACCAACC TGCAGCTCGA GGGCTGCCTC GGGAACAGTA
AGACCGAGGA CCAGCGCAAC

10

1321 GAGGAGAAGG CGCAGCGTGA GGCCAACAAA AAGATCGAGA
AGCAGCTGCA GAAGGACAAG

1381 CAGGTCTACC GGGCCACGCA CCGCCTGCTG CTGCTGGGTG
15 CTGGAGAATC TGGTAAAAGC

1441 ACCATTGTGA AGCAGATGAG GATCCTGCAT GTTAATGGGT
TTAATGGAGA CAGTGAGAAG

1501 GCAACCAAAG TGCAGGACAT CAAAAACAAC CTGAAAGAGG
CGATTGAAAC CATTGTGGCC

1561 GCCATGAGCA ACCTGGTGCC CCCC GTGGAG CTGGCCAACC
20 CCGAGAACCA GTTCAGAGTG

1621 GACTACATCC TGAGTGTGAT GAACGTGCCT GACTTTGACT
TCCCTCCCGA ATTCTATGAG

1681 CATGCCAAGG CTCTGTGGGA GGATGAAGGA GTGCGTGCCT
25 GCTACGAACG CTCCAACGAG

WO 03/072014

PCT/US02/16877

1741 TACCAGCTGA TTGACTGTGC CCAGTACTTC CTGGACAAGA
TCGACGTGAT CAAGCAGGCT

1801 GACTATGTGC CGAGCGATCA GGACCTGCTT CGCTGCCGTG
TCCTGACTTC TGGAATCTTT

5 1861 GAGACCAAGT TCCAGGTGGA CAAAGTCAAC TTCCACATGT
TTGACGTGGG TGGCCAGCGC

1921 GATGAACGCC GCAAGTGGAT CCAGTGCTTC AACGATGTGA
CTGCCATCAT CTTCGTGGTG

10 1981 GCCAGCAGCA GCTACAACAT GGTCATCCGG GAGGACAACC
AGACCAACCG CCTGCAGGAG

2041 GCTCTGAACC TCTTCAAGAG CATCTGGAAC AACAGATGGC
TGCGCACCAT CTCTGTGATC

2101 CTGTTCTCTCA ACAAGCAAGA TCTGCTCGCT GAGAAAGTCC
TTGCTGGGAA ATCGAAGATT

15 2161 GAGGACTACT TTCCAGAATT TGCTCGCTAC ACTACTCCTG
AGGATGCTAC TCCCGAGCCC

2221 GGAGAGGACC CACGCGTGAC CCGGGCCAAG TACTTCATTC
GAGATGAGTT TCTGAGGATC

20 2281 AGCACTGCCA GTGGAGATGG GCGTCACTAC TGCTACCCTC
ATTTCACCTG CGCTGTGGAC

2341 ACTGAGAACA TCCGCCGTGT GTTCAACGAC TGCCGTGACA
TCATTACGCG CATGCACCTT

ClaI Stop XbaI

Stem-loop

25 2401 CGTCAGTACG AGCTGCTCAT CGATTAATAA TCTAGAGGAT
CCCCGCGCCC TCATCCGAAA

WO 03/072014

PCT/US02/16877

2461 GGGCG

5

SEQ ID NO.: 190

Human 2AR stop GS1 transcriptional fusion

10

PstI +1 B2AR

1 GTCGACATGG GGCAACCCGG GAACGGCAGC GCCTTCTTGC
TGGCACCCAA TGGAAGCCAT

15

61 GCGCCGGACC ACGACGTCAC GCAGCAAAGG GACGAGGTGT
GGGTGGTGGG CATGGGCATC

121 GTCATGTCTC TCATCGTCCT GGCCATCGTG TTTGGCAATG
TGCTGGTCAT CACAGCCATT

20

181 GCCAAGTTCG AGCGTCTGCA GACGGTCACC AACTACTTCA
TCACTTCACT GGCCTGTGCT

241 GATCTGGTCA TGGGCCTAGC AGTGGTGCCC TTTGGGGCCG
CCCATATTCT TATGAAAATG

301 TGGACTTTTG GCAACTTCTG GTGCGAGTTT TGGACTTCCA
TTGATGTGCT GTGCGTCACG

WO 03/072014

PCT/US02/16877

361 GCCAGCATTG AGACCCTGTG CGTGATCGCA GTGGATCGCT
ACTTTGCCAT TACTTCACCT

421 TTCAAGTACC AGAGCCTGCT GACCAAGAAT AAGGCCCCGGG
TGATCATTCT GATGGTGTGG

5 481 ATTGTGTCAG GCCTTAYCTC CTTCTTGCCC ATTCAGATGC
ACTGGTACAG GGCCACCCAC

541 CAGGAAGCCA TCAACTGCTA TGCCAATGAG ACCTGCTGTG
ACTTCTTCAC GAACCAAGCC

601 TATGCCATTG CCTCTTCCAT CGTGTCTTC TACGTTCCCC
10 TGGTGATCAT GGTCTTCGTC

661 TACTCCAGGG TCTTTCAGGA GGCCAAAAGG CAGCTCCAGA
AGATTGACAA ATCTGAGGGC

721 CGCTTCCATG TCCAGAACCT TAGCCAGGTG GAGCAGGATG
GGCGGACGGG GCATGGACTC

15 781 CGCAGATCTT CCAAGTTCTG CTTGAAGGAG CACAAAGCCC
TCAAGACGTT AGGCATCATC

841 ATGGGCACTT TCACCCTCTG CTGGCTGCCC TTCTTCATCG
TTAACATTGT GCATGTGATC

901 CAGGATAACC TCATCCGTAA GGAAGTTTAC ATCCTCCTAA
20 ATTGGATAGG CTATGTCAAT

961 TCTGGTTTCA ATCCCCTTAT CTA CTGCGG AGCCCAGATT
TCAGGATTGC CTTCCAGGAG

1021 CTTCTGTGCC TGC GCAGGTC TTCTTTGAAG GCCTATGGCA
ATGGCTACTC CAGCAACGGC

25 1081 AACACAGGGG AGCAGAGTGG ATATCACGTG GAACAGGAGA
AAGAAAATAA ACTGCTGTGT

WO 03/072014

PCT/US02/16877

1141 GAAGACCTCC CAGGCACGGA AGACTTTGTG GGCCATCAAG
GTACTGTGCC TAGCGATAAC

Last B2AR Linker

5 sequence

1201 ATTGATTCAC AAGGGAGGAA TTGTAGTACA AATGACTCAC
TGCTAGAGCG TGGCCAGACG

PstI Stop SD XhoI +2 GS1 alpha

10 1261 GTCACCAACC TGCAGTAATA ATCAAGGAGG CCCTCGAGAT
GGGCTGCCTC GGGAACAGTA

15 1321 AGACCGAGGA CCAGCGCAAC GAGGAGAAGG CGCAGCGTGA
GGCCAACAAA AAGATCGAGA

1381 AGCAGCTGCA GAAGGACAAG CAGGTCTACC GGGCCACGCA
CCGCCTGCTG CTGCTGGGTG

1441 CTGGAGAATC TGGTAAAAGC ACCATTGTGA AGCAGATGAG
GATCCTGCAT GTTAATGGGT

20 1501 TTAATGGAGA CAGTGAGAAG GCAACCAAAG TGCAGGACAT
CAAAAACAAC CTGAAAGAGG

1561 CGATTGAAAC CATTGTGGCC GCCATGAGCA ACCTGGTGCC
CCCCGTGGAG CTGGCCAACC

25 1621 CCGAGAACCA GTTCAGAGTG GACTACATCC TGAGTGTGAT
GAACGTGCCT GACTTTGACT

PCT/US02/16877

1741 GCTACGAACG CTCCAACGAG TACCAGCTGA TTGACTGTGC
CCAGTACTTC CTGGACAAGA

5 1801 TCGACGTGAT CAAGCAGGCT GACTATGTGC CGAGCGATCA
GGACCTGCTT CGCTGCCGTG

1861 TCCTGACTTC TGGAATCTTT GAGACCAAGT TCCAGGTGGA
CAAAGTCAAC TTCCACATGT

1921 TTGACGTGGG TGGCCAGCGC GATGAACGCC GCAAGTGGAT
10 CCAGTGCTTC AACGATGTGA

1981 CTGCCATCAT CTTCGTGGTG GCCAGCAGCA GCTACAACAT
GGTCATCCGG GAGGACAACC

2041 AGACCAACCG CCTGCAGGAG GCTCTGAACC TCTTCAAGAG
CATCTGGAAC AACAGATGGC

15 2101 TGCGCACCAT CTCTGTGATC CTGTTCTCA ACAAGCAAGA
TCTGCTCGCT GAGAAAGTCC

2161 TTGCTGGGAA ATCGAAGATT GAGGACTACT TTCCAGAATT
TGCTCGCTAC ACTACTCCTG

2221 AGGATGCTAC TCCCGAGCCC GGAGAGGACC CACGCGTGAC
20 CCGGGCCAAG TACTTCATTC

2281 GAGATGAGTT TCTGAGGATC AGCACTGCCA GTGGAGATGG
GCGTCACTAC TGCTACCCCTC

2341 ATTTACCTG CGCTGTGGAC ACTGAGAACA TCCGCCGTGT
GTTCAACGAC TGCCGTGACA

ClaI Stop XbaI

WO 03/072014

PCT/US02/16877

2401 TCATTCAGCG CATGCACCTT CGTCAGTACG AGCTGCTCAT
CGATTAATAA TCTAGAGGAT

Stem-loop

5 2461 CCCC GCGCCC TCATCCGAAA GGGCG

SEQ ID NO.: 192

10

Human GS1

XhoI

1

15 CTCGAGATGGGCTGCCTCGGGAACAGTAAGACCGAGGACCAGCGCAACGAGGAG
AAGGCGCAGCGT

1 M G C L G N S K T E D Q R N E E K A Q R

61

20 GAGGCCAACAAAAAGATCGAGAAGCAGCTGCAGAAGGACAAGCAGGTCTACCGG
GCCACG

21 E A N K K I E K Q L Q K D K Q V Y R A T

PCT/US02/16877

CACCGCCTGCTGCTGCTGGGTGCTGGAGAATCTGGTAAAAGCACCATTGTGAAGC
AGATG

5

AGGATCCTGCATGTTAATGGGTTTAATGGAGACAGTGAGAAGGCAACCAAAGTGC
AGGAC

10

ATCAAAAACAACCTGAAAGAGGCGATTGAAACCATTGTGGCCGCCATGAGCAACC
TGGTG

15

CCCCCGTGGAGCTGGCCAACCCGAGAACCAGTTCAGAGTGGACTACATCCTGA
GTGTG

20

ATGAACGTGCCTGACTTTGACTTCCCTCCCGAATTCTATGAGCATGCCAAGGCTCT
GTGG

25

WO 03/072014

PCT/US02/16877

421

GAGGATGAAGGAGTGCCTGCCTGCTACGAACGCTCCAACGAGTACCAGCTGATTG
ACTGT

141 E D E G V R A C Y E R S N E Y Q L I D C

5

481

GCCCAGTACTTCCTGGACAAGATCGACGTGATCAAGCAGGCTGACTATGTGCCGA
GCGAT

161 A Q Y F L D K I D V I K Q A D Y V P S D

10

541

CAGGACCTGCTTCGCTGCCGTGTCCTGACTTCTGGAATCTTTGAGACCAAGTTCCA
GGTG

181 Q D L L R C R V L T S G I F E T K F Q V

15

601

GACAAAGTCAACTTCCACATGTTTGACGTGGGTGGCCAGCGCGATGAACGCCGCA
AGTGG

201 D K V N F H M F D V G G Q R D E R R K W

20

661

ATCCAGTGCTTCAACGATGTGACTGCCATCATCTTCGTGGTGGCCAGCAGCAGCTA
CAAC

221 I Q C F N D V T A I I F V V A S S S Y N

25

WO 03/072014

PCT/US02/16877

721

ATGGTCATCCGGGAGGACAACCAGACCAACCGCCTGCAGGAGGCTCTGAACCTCT
TCAAG

241 M V I R E D N Q T N R L Q E A L N L F K

5

781

AGCATCTGGAACAACAGATGGCTGCGCACCATCTCTGTGATCCTGTTCTCAACA
AGCAA

261 S I W N N R W L R T I S V I L F L N K Q

10

841

GATCTGCTCGCTGAGAAAGTCCTTGCTGGGAAATCGAAGATTGAGGACTACTTTC
CAGAA

281 D L L A E K V L A G K S K I E D Y F P E

15

901

TTTGCTCGCTACACTACTCCTGAGGATGCTACTCCCGAGCCCGGAGAGGACCCAC
GCGTG

301 F A R Y T T P E D A T P E P G E D P R V

20

961

ACCCGGGCCAAGTACTTCATTGAGATGAGTTTCTGAGGATCAGCACTGCCAGTG
GAGAT

321 T R A K Y F I R D E F L R I S T A S G D

25

WO 03/072014

PCT/US02/16877

1021

GGGCGTCACTACTGCTACCCTCATTTACCTGCGCTGTGGACACTGAGAACATCCG
CCGT

341 G R H Y C Y P H F T C A V D T E N I R R

5

1081

GTGTTCAACGACTGCCGTGACATCATTACGCGCATGCACCTTCGTCAGTACGAGCT
GCTC

361 V F N D C R D I I Q R M H L R Q Y E L L

10

ClaI

ATCGAT

15

SEQ ID NO.: 193

Human GS2

XhoI

20

1

CTCGAGATGGGCTGCCTCGGGAACAGTAAGACCGAGGACCAGCGCAACGAGGAG
AAGGCGCAGCGT

1 M G C L G N S K T E D Q R N E E K A Q R

WO 03/072014

PCT/US02/16877

61

GAGGCCAACAAAAAGATCGAGAAGCAGCTGCAGAAGGACAAGCAGGTCTACCGG
GCCACG

21 E A N K K I E K Q L Q K D K Q V Y R A T

5

121

CACCGCCTGCTGCTGCTGGGTGCTGGAGAATCTGGTAAAAGCACCATTGTGAAGC
AGATG

41 H R L L L L G A G E S G K S T I V K Q M

10

181

AGGATCCTGCATGTTAATGGGTTTAATGGAGAGGGCGGCGAAGAGGACCCGCAGG
CTGCA

61 R I L H V N G F N G E G G E E D P Q A A

15

241

AGGAGCAACAGCGATGGTGAGAAGGCAACCAAAGTGCAGGACATCAAAAACAAC
CTGAAA

81 R S N S D G E K A T K V Q D I K N N L K

20

301

GAGGCGATTGAAACCATTGTGGCCGCCATGAGCAACCTGGTGCCCCCGTGGAGC
TGGCC

101 E A I E T I V A A M S N L V P P V E L A

25

WO 03/072014

PCT/US02/16877

361

AACCCCGAGAACCAGTTCAGAGTGGACTACATCCTGAGTGTGATGAACGTGCCTG
ACTTT

121 N P E N Q F R V D Y I L S V M N V P D F

5

421

GACTTCCCTCCCGAATTCTATGAGCATGCCAAGGCTCTGTGGGAGGATGAAGGAG
TGCGT

141 D F P P E F Y E H A K A L W E D E G V R

10

481

GCCTGCTACGAACGCTCCAACGAGTACCAGCTGATTGACTGTGCCCAGTACTTCCT
GGAC

161 A C Y E R S N E Y Q L I D C A Q Y F L D

15

541

AAGATCGACGTGATCAAGCAGGCTGACTATGTGCCGAGCGATCAGGACCTGCTTC
GCTGC

181 K I D V I K Q A D Y V P S D Q D L L R C

20

601

CGTGTCTGACTTCTGGAATCTTTGAGACCAAGTTCCAGGTGGACAAAGTCAACTT
CCAC

201 R V L T S G I F E T K F Q V D K V N F H

25

WO 03/072014

PCT/US02/16877

661

ATGTTTGACGTGGGTGGCCAGCGCGATGAACGCCGCAAGTGGATCCAGTGCTTCA
ACGAT

221 M F D V G G Q R D E R R K W I Q C F N D

5

721

GTGACTGCCATCATCTTCGTGGTGGCCAGCAGCAGCTACAACATGGTCATCCGGG
AGGAC

241 V T A I I F V V A S S S Y N M V I R E D

10

781

AACCAGACCAACCGCCTGCAGGAGGCTCTGAACCTCTTCAAGAGCATCTGGAACA
ACAGA

261 N Q T N R L Q E A L N L F K S I W N N R

15

841

TGGCTGCGCACCATCTCTGTGATCCTGTTCCCTCAACAAGCAAGATCTGCTCGCTGA
GAAA

281 W L R T I S V I L F L N K Q D L L A E K

20

901

GTCCTTGCTGGGAAATCGAAGATTGAGGACTACTTTCCAGAATTTGCTCGCTACAC
TACT

301 V L A G K S K I E D Y F P E F A R Y T T

25

WO 03/072014

PCT/US02/16877

961

CCTGAGGATGCTACTCCCGAGCCCGGAGAGGACCCACGCGTGACCCGGGCCAAGT
ACTTC

321 P E D A T P E P G E D P R V T R A K Y F

5

1021

ATTCGAGATGAGTTTCTGAGGATCAGCACTGCCAGTGGAGATGGGCGTCACTACT
GCTAC

341 I R D E F L R I S T A S G D G R H Y C Y

10

1081

CCTCATTTACCTGCGCTGTGGACACTGAGAACATCCGCCGTGTGTTCAACGACTG
CCGT

361 P H F T C A V D T E N I R R V F N D C R

15

C1aI

1141

GACATCATTCAGCGCATGCACCTTCGTCAGTACGAGCTGCTCATCGAT

381 D I I Q R M H L R Q Y E L L

20

SEQ ID NO.: 194

WO 03/072014

PCT/US02/16877

Human G q

XhoI

1

5 CTCGAGATGACTCTGGAGTCCATCATGGCGTGCTGCCTGAGCGAGGAGGCCAAGG
AAGCCCGGCGG

1 M T L E S I M A C C L S E E A K E A R R

61

10 ATCAACGACGAGATCGAGCGGCAGCTCCGCAGGGACAAGCGGGACGCCCGCCGG
GAGCTC

21 I N D E I E R Q L R R D K R D A R R E L

121

15 AAGCTGCTGCTGCTCGGGACAGGAGAGAGTGGCAAGAGTACGTTTATCAAGCAGA
TGAGA

41 K L L L L G T G E S G K S T F I K Q M R

181

20 ATCATCCATGGGTCAGGATACTCTGATGAAGATAAAAGGGGCTTCACCAAGCTGG
TGTAT

61 I I H G S G Y S D E D K R G F T K L V Y

PCT/US02/16877

CAGAACATCTTCACGGCCATGCAGGCCATGATCAGAGCCATGGACACACTCAAGA
TCCCA

5

TACAAGTATGAGCACAATAAGGCTCATGCACAATTAGTTCGAGAAGTTGATGTGG
AGAAG

10

GTGTCTGCTTTTGAGAATCCATATGTAGATGCAATAAAGAGTTTATGGAATGATCC
TGGA

15

ATCCAGGAATGCTATGATAGACGACGAGAATATCAATTATCTGACTCTACCAAAT
ACTAT

20

CTTAATGACTTGGACCGCGTAGCTGACCCTGCCTACCTGCCTACGCAACAAGATGT
GCTT

25

WO 03/072014

PCT/US02/16877

541

AGAGTTCGAGTCCCCACCACAGGGATCATCGAATACCCCTTTGACTTACAAAGTG
TCATT

181 R V R V P T T G I I E Y P F D L Q S V I

5

601

TTCAGAATGGTCGATGTAGGGGGCCAAAGGTCAGAGAGAAGAAAATGGATACACT
GCTTT

201 F R M V D V G G Q R S E R R K W I H C F

10

661

GAAAATGTCACCTCTATCATGTTTCTAGTAGCGCTTAGTGAATATGATCAAGTTCT
CGTG

221 E N V T S I M F L V A L S E Y D Q V L V

15

721

GAGTCAGACAATGAGAACCGAATGGAGGAAAGCAAGGCTCTCTTTAGAACAATTA
TCACA

241 E S D N E N R M E E S K A L F R T I I T

20

781

TACCCCTGGTTCCAGAACTCCTCGGTTATTCTGTTCTTAAACAAGAAAGATCTTCT
AGAG

261 Y P W F Q N S S V I L F L N K K D L L E

25

PCT/US02/16877

GAGAAAATCATGTATTCCCATCTAGTCGACTACTTCCCAGAATATGATGGACCCC
AGAGA

5

GATGCCAGGCAGCCCGAGAATTCATTCTGAAGATGTTCTGGACCTGAACCCAG
ACAGT

10

GACAAAATTATCTACTCCCAC TTCACGTGCGCCACAGACACCGAGAATATCCGCT
TTGTC

15

1021

TTTGCTGCCGTCAAGGACACCATCCTCCAGTTGAACCTGAAGGAGTACAATCTGG
TCATCGAT

25

SEQ ID NO.: 195

WO 03/072014

PCT/US02/16877

Human Gi

XhoI

5 1
CTCGAGATGGGCTGCACCGTGAGCGCCGAGGACAAGGCGGCGGCCGAGCGCTCTA
AGATGATCGAC

1 M G C T V S A E D K A A A E R S K M I D

10 61
AAGAACCTGCGGGAGGACGGAGAGAAGGCGGCGCGGGAGGTGAAGTTGCTGCTG
TTGGGT

21 K N L R E D G E K A A R E V K L L L L G

15 121
GCTGGGGAGTCAGGGAAGAGCACCATCGTCAAGCAGATGAAGATCATCCACGAG
GATGGC

41 A G E S G K S T I V K Q M K I I H E D G

20 181
TACTCCGAGGAGGAATGCCGGCAGTACCGGGCGGTTGTCTACAGCAACACCATCC
AGTCC

61 Y S E E E C R Q Y R A V V Y S N T I Q S

WO 03/072014

PCT/US02/16877

241

ATCATGGCCATTGTCAAAGCCATGGGAAACCTGCAGATCGACTTTGCCGACCCCT
CCAGA

81 I M A I V K A M G N L Q I D F A D P S R

5

301

GCGGACGACGCCAGGCAGCTATTTGCACTGTCCTGCACCGCCGAGGAGCAAGGCG
TGCTC

101 A D D A R Q L F A L S C T A E E Q G V L

10

361

CCTGATGACCTGTCCGGCGTCATCCGGAGGCTCTGGGCTGACCATGGTGTGCAGG
CCTGC

121 P D D L S G V I R R L W A D H G V Q A C

15

421

TTTGGCCGCTCAAGGGAATACCAGCTCAACGACTCAGCTGCCTACTACCTGAACG
ACCTG

141 F G R S R E Y Q L N D S A A Y Y L N D L

20

481

GAGCGTATTGCACAGAGTGACTACATCCCCACACAGCAAGATGTGCTACGGACCC
GCGTA

161 E R I A Q S D Y I P T Q Q D V L R T R V

25

PCT/US02/16877

181 K T T G I V E T H F T F K D L H F K M F

201 D V G G Q R S E R K K W I H C F E G V T

221 A I I F C V A L S A Y D L V L A E D E E

241 M N R M H E S M K L F D S I C N N K W F

261 T D T S I I L F L N K K D L F E E K I T

131/268

WO 03/072014

PCT/US02/16877

841

CACAGTCCCCTGACCATCTGCTTCCCTGAGTACACAGGGGCCAACAAATATGATG
AGGCA

281 H S P L T I C F P E Y T G A N K Y D E A

5

901

GCCAGCTACATCCAGAGTAAGTTTGAGGACCTGAATAAGCGCAAAGACACCAAGG
AGATC

301 A S Y I Q S K F E D L N K R K D T K E I

10

961

TACACGCACTTCACGTGCGCCACCGACACCAAGAACGTGCAGTTCGTGTTTGACG
CCGTC

321 Y T H F T C A T D T K N V Q F V F D A V

15

ClaI

1021

ACCGATGTCATCATCAAGAACAACCTGAAGGACTGCGGCCTCTTCATGCAT

341 T D V I I K N N L K D C G L F

20

SEQ ID NO.: 196

PCT/US02/16877

XhoI

5 CTCGAGATGTCCGGGGTGGTGCGGACCCTCAGCCGCTGCCTGCTGCCGGCCGAGG
CCGGCGGGGCC

61

10 CGCGAGCGCAGGGCGGGCAGCGGCGCGCGACGCGGAGCGCGAGGCCCGGAGG
CGTAGC

21 R E R R A G S G A R D A E R E A R R R S

121

15 CGCGACATCGACGCGCTGCTGGCCGCGAGCGGCGCGCGGTCCGGCGCCTGGTGA
AGATC

41 R D I D A L L A R E R R A V R R L V K I

181

20 CTGCTGCTGGGCGCGGGCGAGAGCGGCAAGTCCACGTTCCCTCAAGCAGATGCGCA
TCATC

61 L L L G A G E S G K S T F L K Q M R I I

WO 03/072014

PCT/US02/16877

241

CACGGCCGCGAGTTCGACCAGAAGGCGCTGCTGGAGTTCCGCGACACCATCTTCG
ACAAC

81 H G R E F D Q K A L L E F R D T I F D N

5

301

ATCCTCAAGGGCTCAAGGGTTCTTGTTGATGCACGAGATAAGCTTGGCATTCTCTG
GCAG

101 I L K G S R V L V D A R D K L G I P W Q

10

361

TATTCTGAAAATGAGAAGCATGGGATGTTCTGATGGCCTTCGAGAACAAGGCGG
GGCTG

121 Y S E N E K H G M F L M A F E N K A G L

15

421

CCTGTGGAGCCGGCCACCTTCCAGCTGTACGTCCCGGCCCTGAGCGCACTCTGGA
GGGAT

141 P V E P A T F Q L Y V P A L S A L W R D

20

481

TCTGGCATCAGGGAGGCTTTCAGCCGGAGAAGCGAGTTTCAGCTGGGGGAGTCGG
TGAAG

161 S G I R E A F S R R S E F Q L G E S V K

25

WO 03/072014

PCT/US02/16877

541

TACTTCCTGGACAACTTGGACCGGATCGGCCAGCTGAATTACTTTCCTAGTAAGCA
AGAT

181 Y F L D N L D R I G Q L N Y F P S K Q D

5

601

ATCCTGCTGGCTAGGAAAGCCACCAAGGGAATTGTGGAGCATGACTTCGTTATTA
AGAAG

201 I L L A R K A T K G I V E H D F V I K K

10

661

ATCCCCTTTAAGATGGTGGATGTGGGCGGCCAGCGGTCCCAGCGCCAGAAGTGGT
TCCAG

221 I P F K M V D V G G Q R S Q R Q K W F Q

15

721

TGCTTCGACGGGATCACGTCCATCCTGTTCATGGTCTCCTCCAGCGAGTACGACCA
GGTC

241 C F D G I T S I L F M V S S S E Y D Q V

20

781

CTCATGGAGGACAGGCGCACCAACCGGCTGGTGGAGTCCATGAACATCTTCGAGA
CCATC

261 L M E D R R T N R L V E S M N I F E T I

25

WO 03/072014

PCT/US02/16877

841

GTCAACAACAAGCTCTTCTTCAACGTCTCCATCATTCTTCTCCTCAACAAGATGGA
CCTC

281 V N N K L F F N V S I I L F L N K M D L

5

901

CTGGTGGAGAAGGTGAAGACCGTGAGCATCAAGAAGCACTTCCCGGACTTCAGGG
GCGAC

301 L V E K V K T V S I K K H F P D F R G D

10

961

CCGCACCAGCTGGAGGACGTCCAGCGCTACCTGGTCCAGTGCTTCGACAGGAAGA
GACGG

321 P H Q L E D V Q R Y L V Q C F D R K R R

15

1021

AACCGCAGCAAGCCACTCTTCCACCACTTCACCACCGCCATCGACACCGAGAACG
TCCGC

341 N R S K P L F H H F T T A I D T E N V R

20

1081

TTCGTGTTCCATGCTGTGAAAGACACCATCCTGCAGGAGAACCTGAAGGACATCA
TGCTG

361 F V F H A V K D T I L Q E N L K D I M L

25

WO 03/072014

PCT/US02/16877

ClaI

1141 CAGATCGAT

381 Q

5

10

SEQ ID NO.: 205

15

Human 2AR-ToxR (5-141) chimera stop GS1 -ToxR (5-141) chimera transcriptional
fusion

SalI +1 B2AR

20 1 GTCGACATGG GGCAACCCGG GAACGGCAGC GCCTTCTTGC
TGGCACCCAA TGGAAGCCAT

WO 03/072014

PCT/US02/16877

61 GCGCCGGACC ACGACGTCAC GCAGCAAAGG GACGAGGTGT
GGGTGGTGGG CATGGGCATC

121 GTCATGTCTC TCATCGTCCT GGCCATCGTG TTTGGCAATG
5 TGCTGGTCAT CACAGCCATT

181 GCCAAGTTCG AGCGTCTGCA GACGGTCACC AACTACTTCA
TCACTTCACT GGCCTGTGCT

241 GATCTGGTCA TGGGCCTAGC AGTGGTGCCC TTTGGGGCCG
CCCATATTCT TATGAAAATG

10 301 TGGACTTTTG GCAACTTCTG GTGCGAGTTT TGGACTTCCA
TTGATGTGCT GTGCGTCACG

361 GCCAGCATTG AGACCCTGTG CGTGATCGCA GTGGATCGCT
ACTTTGCCAT TACTTCACCT

421 TTCAAGTACC AGAGCCTGCT GACCAAGAAT AAGGCCCGGG
15 TGATCATTCT GATGGTGTGG

481 ATTGTGTCAG GCCTTAYCTC CTTCTTGCCC ATTCAGATGC
ACTGGTACAG GGCCACCCAC

541 CAGGAAGCCA TCAACTGCTA TGCCAATGAG ACCTGCTGTG
ACTTCTTCAC GAACCAAGCC

20 601 TATGCCATTG CCTCTTCCAT CGTGTCTTTC TACGTTCCCC
TGGTGATCAT GGTCTTCGTC

661 TACTCCAGGG TCTTTCAGGA GGCCAAAAGG CAGCTCCAGA
AGATTGACAA ATCTGAGGGC

721 CGCTTCCATG TCCAGAACCT TAGCCAGGTG GAGCAGGATG
25 GGCGGACGGG GCATGGACTC

WO 03/072014

PCT/US02/16877

781 CGCAGATCTT CCAAGTTCTG CTTGAAGGAG CACAAAGCCC
TCAAGACGTT AGGCATCATC

841 ATGGGCACTT TCACCCTCTG CTGGCTGCCC TTCTTCATCG
TTAACATTGT GCATGTGATC

5 901 CAGGATAACC TCATCCGTAA GGAAGTTTAC ATCCTCCTAA
ATTGGATAGG CTATGTCAAT

961 TCTGGTTTCA ATCCCCTTAT CTACTGCCGG AGCCCAGATT
TCAGGATTGC CTTCCAGGAG

1021 CTTCTGTGCC TGC GCAGGTC TTCTTTGAAG GCCTATGGCA
10 ATGGCTACTC CAGCAACGGC

1081 AACACAGGGG AGCAGAGTGG ATATCACGTG GAACAGGAGA
AAGAAAATAA ACTGCTGTGT

1141 GAAGACCTCC CAGGCACGGA AGACTTTGTG GGCCATCAAG
GTACTGTGCC TAGCGATAAC

15

last B2AR linker

sequence

1201 ATTGATTCAC AAGGGAGGAA TTGTAGTACA AATGACTCAC
TGCTAGAGCG TGGCCAGACG

20

PstI +5 toxR (5-141)

1261 GTCACCAACC TGCAGGGACA CAACTCAAAA GAGATATCGA
TGAGTCATAT TGGTACTAAA

25

WO 03/072014

PCT/US02/16877

1321 TTCATTCTTG CTGAAAAATT TACCTTCGAT CCCCTAAGCA
ATACTCTGAT TGACAAAGAA

1381 GATAGTGAAG AGATCATTCG ATTAGGCAGC AACGAAAGCC
GAATTCTTTG GCTGCTGGCC

5 1441 CAACGTCCAA ACGAGGTAAT TTCTCGCAAT GATTTGCATG
ACTTTGTTTG GCGAGAGCAA

1501 GGTTTTGAAG TCGATGATTC CAGCTTAACC CAAGCCATTT
CGACTCTGCG CAAAATGCTC

1561 AAAGATTCGA CAAAGTCCCC ACAATACGTC AAAACGGTTC
10 CGAAGCGCGG TTACCAATTG

1621 ATCGCCCGAG TGGAAACGGT TGAAGAAGAG ATGGCTCGCG
AAAACGAAGC TGCTCATGAC

stop SD XhoI +1 GS1 alpha

15 1681 ATCTCTTAAT AATCAAGGAG GCCCTCGAGA TGGGCTGCCT
CGGGAACAGT AAGACCGAGG

1741 ACCAGCGCAA CGAGGAGAAG GCGCAGCGTG AGGCCAACAA
20 AAAGATCGAG AAGCAGCTGC

1801 AGAAGGACAA GCAGGTCTAC CGGGCCACGC ACCGCCTGCT
GCTGCTGGGT GCTGGAGAAT

1861 CTGGTAAAAG CACCATTGTG AAGCAGATGA GGATCCTGCA
TGTTAATGGG TTTAATGGAG

25 1921 ACAGTGAGAA GGCAACCAAA GTGCAGGACA TCAAAAACAA
CCTGAAAGAG GCGATTGAAA

WO 03/072014

PCT/US02/16877

1981 CCATTGTGGC CGCCATGAGC AACCTGGTGC CCCCCGTGGA
GCTGGCCAAC CCCGAGAACC

2041 AGTTCAGAGT GGACTACATC CTGAGTGTGA TGAACGTGCC
TGACTTTGAC TTCCCTCCCG

5 2101 AATTCTATGA GCATGCCAAG GCTCTGTGGG AGGATGAAGG
AGTGCGTGCC TGCTACGAAC

2161 GCTCCAACGA GTACCAGCTG ATTGACTGTG CCCAGTACTT
CCTGGACAAG ATCGACGTGA

2221 TCAAGCAGGC TGACTATGTG CCGAGCGATC AGGACCTGCT
10 TCGCTGCCGT GTCCTGACTT

2281 CTGGAATCTT TGAGACCAAG TTCCAGGTGG ACAAAGTCAA
CTTCCACATG TTTGACGTGG

2341 GTGGCCAGCG CGATGAACGC CGCAAGTGGA TCCAGTGCTT
CAACGATGTG ACTGCCATCA

15 2401 TCTTCGTGGT GGCCAGCAGC AGCTACAACA TGGTCATCCG
GGAGGACAAC CAGACCAACC

2461 GCCTGCAGGA GGCTCTGAAC CTCTTCAAGA GCATCTGGAA
CAACAGATGG CTGCGCACCA

2521 TCTCTGTGAT CCTGTTCCCTC AACAAGCAAG ATCTGCTCGC
20 TGAGAAAGTC CTTGCTGGGA

2581 AATCGAAGAT TGAGGACTAC TTTCCAGAAT TTGCTCGCTA
CACTACTCCT GAGGATGCTA

2641 CTCCCGAGCC CGGAGAGGAC CCACGCGTGA CCCGGGCCAA
GTACTTCATT CGAGATGAGT

25 2701 TTCTGAGGAT CAGCACTGCC AGTGGAGATG GGCCTCACTA
CTGCTACCCT CATTTCACCT

WO 03/072014

PCT/US02/16877

2761 GCGCTGTGGA CACTGAGAAC ATCCGCCGTG TGTTCACGA
CTGCCGTGAC ATCATTACGC

ClaI +5 toxR (5-141)

5 2821 GCATGCACCT TCGTCAGTAC GAGCTGCTCA TCGATGGACA
CAACTCAAAA GAGATATCGA

2881 TGAGTCATAT TGGTACTAAA TTCATTCTTG CTGAAAAATT
10 TACCTTCGAT CCCCTAAGCA

2941 ATACTCTGAT TGACAAAGAA GATAGTGAAG AGATCATTCTG
ATTAGGCAGC AACGAAAGCC

3001 GAATTCTTTG GCTGCTGGCC CAACGTCCAA ACGAGGTAAT
TTCTCGCAAT GATTTGCATG

15 3061 ACTTTGTTTG GCGAGAGCAA GGTTTGAAG TCGATGATTC
CAGCTTAACC CAAGCCATTT

3121 CGACTCTGCG CAAAATGCTC AAAGATTCTGA CAAAGTCCCC
ACAATACGTC AAAACGGTTC

3181 CGAAGCGCGG TTACCAATTG ATCGCCCGAG TGGAAACGGT
20 TGAAGAAGAG ATGGCTCGCG

Stop XbaI

Stem-loop

3241 AAAACGAAGC TGCTCATGAC ATCTCTTAAT AATCTAGAGG
25 ATCCCCGCGC CCTCATCCGA

WO 03/072014

PCT/US02/16877

3301 AAGGGCG

5

SEQ ID NO.: 208

Vibrio cholerae Pctx::lacZ reporter fusion construct

10

XbaI

1 TCTAGAGGCT GTGGGTAGAA GTGAAACGGG GTTTACCGAT
AAAAACAGAA AATGATAAAA

3 ToxR binding repeats

15

61 AAGGACTAAA TAGTATATTT TGATTTTGA TTTTGATT
CAAATAATAC AAATTTATTT

+1 lacZ

20

121 ACTTATTTAA TTGTTTGTAT CAATTATTT TCTGTAAAC
AAAGGGAGCA TTATATGGTA

WO 03/072014

PCT/US02/16877

181 AAGACCATGA TTACGGATTC ACTGGCCGTC GTTTTACAAC
GTCGTGACTG GGAAAACCCT

241 GCGTTACCC AACTTAATCG CCTTGCAGCA CATCCCCCTT
TCGCCAGCTG GCGTAATAGC

5 301 GAAGAGGCCC GCACCGATCG CCCTTCCCAA CAGTTGCGCA
GCCTGAATGG CGAATGGCGC

361 TTTGCCTGGT TTCCGGCACC AGAAGCGGTG CCGGAAAGCT
GGCTGGAGTG CGATCTTCCT

421 GAGGCCGATA CTGTCGTCGT CCCCTCAAAC TGGCAGATGC
10 ACGGTTACGA TGCGCCCATC

481 TACACCAACG TGACCTATCC CATTACGGTC AATCCGCCGT
TTGTTCCAC GGAGAATCCG

541 ACGGGTTGTT ACTCGCTCAC ATTTAATGTT GATGAAAGCT
GGCTACAGGA AGGCCAGACG

15 601 CGAATTATTT TTGATGGCGT TAACTCGGCG TTTCATCTGT
GGTGCAACGG GCGCTGGGTC

661 GGTTACGGCC AGGACAGTCG TTTGCCGTCT GAATTTGACC
TGAGCGCATT TTTACGCGCC

721 GGAGAAAACC GCCTCGCGGT GATGGTGCTG CGCTGGAGTG
20 ACGGCAGTTA TCTGGAAGAT

781 CAGGATATGT GGC GGATGAG CGGCATTTTC CGTGACGTCT
CGTTGCTGCA TAAACCGACT

841 ACACAAATCA GCGATTCCA TGTTGCCACT CGCTTTAATG
ATGATTTTCA CCGCGCTGTA

25 901 CTGGAGGCTG AAGTTCAGAT GTGCGGCGAG TTGCGTGACT
ACCTACGGGT AACAGTTTCT

WO 03/072014

PCT/US02/16877

961 TTATGGCAGG GTGAAACGCA GGTCGCCAGC GGCACCGCGC
CTTTCGGCGG TGAAATTATC

1021 GATGAGCGTG GTGGTTATGC CGATCGCGTC AACTACGTC
TGAAACGTCGA AAACCCGAAA

5 1081 CTGTGGAGCG CCGAAATCCC GAATCTCTAT CGTGCGGTGG
TTGAACTGCA CACCGCCGAC

1141 GGCACGCTGA TTGAAGCAGA AGCCTGCGAT GTCGGTTTCC
GCGAGGTGCG GATTGAAAAT

1201 GGTCTGCTGC TGCTGAACGG CAAGCCGTTG CTGATTGAG
10 GCGTTAACCG TCACGAGCAT

1261 CATCCTCTGC ATGGTCAGGT CATGGATGAG CAGACGATGG
TGCAGGATAT CCTGCTGATG

1321 AAGCAGAACA ACTTTAACGC CGTGCGCTGT TCGCATTATC
CGAACCATCC GCTGTGGTAC

15 1381 ACGCTGTGCG ACCGCTACGG CCTGTATGTG GTGGATGAAG
CCAATATTGA AACCCACGGC

1441 ATGGTGCCAA TGAATCGTCT GACCGATGAT CCGCGCTGGC
TACCGGCGAT GAGCGAACGC

1501 GTAACGCGAA TGGTGCAGCG CGATCGTAAT CACCCGAGTG
20 TGATCATCTG GTCGCTGGGG

1561 AATGAATCAG GCCACGGCGC TAATCACGAC GCGCTGTATC
GCTGGATCAA ATCTGTCGAT

1621 CCTTCCCGCC CGGTGCAGTA TGAAGGCGGC GGAGCCGACA
CCACGGCCAC CGATATTATT

25 1681 TGCCCGATGT ACGCGCGCGT GGATGAAGAC CAGCCCTTCC
CGGCTGTGCC GAAATGGTCC

PCT/US02/16877

1741 ATCAAAAAAT GGCTTTCGCT ACCTGGAGAG ACGCGCCCGC
TGATCCTTTG CGAATACGCC

1801 CACGCGATGG GTAACAGTCT TGGCGGTTTC GCTAAATACT
GGCAGGCGTT TCGTCAGTAT

5 1861 CCCCGTTTAC AGGGCGGCTT CGTCTGGGAC TGGGTGGATC
AGTCGCTGAT TAAATATGAT

1921 GAAAACGGCA ACCCGTGGTC GGCTTACGGC GGTGATTTTG
GCGATACGCC GAACGATCGC

1981 CAGTTCTGTA TGAACGGTCT GGTCTTTGCC GACCGCACGC
10 CGCATCCAGC GCTGACGGAA

2041 GCAAAACACC AGCAGCAGTT TTTCCAGTTC CGTTTATCCG
GGCAAACCAT CGAAGTGACC

2101 AGCGAATACC TGTTCCGTCA TAGCGATAAC GAGCTCCTGC
ACTGGATGGT GGCCTGGAT

15 2161 GGTAAGCCGC TGGCAAGCGG TGAAGTGCCT CTGGATGTCG
 CTCCACAAGG TAAACAGTTG

2221 ATTGAAGTGC CTGAACTACC GCAGCCGGAG AGCGCCGGGC
AACTCTGGCT CACAGTACGC

2281 GTAGTGCAAC CGAACGCGAC CGCATGGTCA GAAGCCGGGC
20 ACATCAGCGC CTGGCAGCAG

2341 TGGCGTCTGG CGGAAAACCT CAGTGTGACG CTCCCCGCCG
CGTCCCACGC CATCCCGCAT

2401 CTGACCACCA GCGAAATGGA TTTTGCATC GAGCTGGGTA
ATAAGCGTTG GCAATTTAAC

25 2461 CGCCAGTCAG GCTTTCTTTC ACAGATGTGG ATTGGCGATA
AAAAACAAC TCTGACGCCG

WO 03/072014

PCT/US02/16877

2521 CTGCGCGATC AGTTCACCCG TGCACCGCTG GATAACGACA
TTGGCGTAAG TGAAGCGACC

2581 CGCATTGACC CTAACGCCTG GGTCGAACGC TGGAAGGCGG
CGGGCCATTA CCAGGCCGAA

5 2641 GCAGCGTTGT TGCAGTGCAC GGCAGATACA CTTGCTGATG
CGGTGCTGAT TACGACCGCT

2701 CACGCGTGGC AGCATCAGGG GAAAACCTTA TTTATCAGCC
GGAAAACCTA CCGGATTGAT

2761 GGTA GTGGTC AAATGGCGAT TACCGTTGAT GTTGAAGTGG
10 CGAGCGATAC ACCGCATCCG

2821 GCGCGGATTG GCCTGAACTG CCAGCTGGCG CAGGTAGCAG
AGCGGGTAAA CTGGCTCGGA

2881 TTAGGGCCGC AAGAAAATA TCCCGACCGC CTTACTGCCG
CCTGTTTTGA CCGCTGGGAT

15 2941 CTGCCATTGT CAGACATGTA TACCCCGTAC GTCTTCCCGA
GCGAAAACGG TCTGCGCTGC

3001 GGGACGCGCG AATTGAATTA TGGCCACAC CAGTGGCGCG
GCGACTTCCA GTTCAACATC

3061 AGCCGCTACA GTCAACAGCA ACTGATGGAA ACCAGCCATC
20 GCCATCTGCT GCACGCGGAA

3121 GAAGGCACAT GGCTGAATAT CGACGGTTTC CATATGGGGA
TTGGTGGCGA CGACTCCTGG

3181 AGCCCGTCAG TATCGGCGGA ATTCCAGCTG AGCGCCGGTC
GCTACCATTA CCAGTTGGTC

25

Stop Stem-loop XbaI

WO 03/072014

PCT/US02/16877

3241 TGGTGTCAAA AATAATAACGCCCTCAT CCGAAAGGGC GTCTAGA

SEQ ID NO.: 266

5

pMPX-74 MalE (1-28) fusion vector

SD old PstI +1

2401

10 GAATTCAGGCGCTTTT TAGACTGGTCGTAATGAAATTCAGGAGGTTCTGCATATGA
AAAT

1

M K I

2461

15 AAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCC
GCCTC

4

K T G A R I L A L S A L T T M M F S A S

Factor Xa PstI SalI XbaI

20

2521

GGCTCTCGCCAAAATCATCGAAGCCCGCCTGCAGGCCTCGGTCGACGCCGAATCT
AGAGA

24

A L A K I I E A R L Q A S V D A E S R D

PCT/US02/16877

lost XbaI

(transcriptional stop)

44 Y K D D D D K

5

Rhamnose inducible, clone into PstI, SalI, XbaI

10 Made by cutting TOPO NsiI-malE (1-28)::FXa::PstI, SalI, XbaI::FLAG-NheI
insertion with NsiI & NheI and cloning into pMPX-72 cut with PstI & XbaI.

15 SEQ ID NO.: 267

pMPX-75 MalE (1-28) fusion vector

SD old PstI +1

20 1621
CCATACCCGTTTTTTGGGCTAGCAGGAGGCCCTGCATATGAAAATAAAAACAGG
TGCAC

1 M K I K T G A

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1681

GCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTCGGCTCTCGCC
AAAA

5 8 R I L A L S A L T T M M F S A S A L A K

Factor Xa PstI

SalI

XbaI

FLAG

1741

10 TCATCGAAGCCCGCCTGCAGGCCTCGGTCGACGCCGAATCTAGAGATTATAAAGA
TGACG

Lost XbaI

1801 ATGACAAATAATAAGCTAGAGG (Transcriptional stop)

15

pMPX-71::malE(1-28)::FXa::PstI, SalI, XbaI::FLAG

Arabinose inducible, clone into PstI, SalI, XbaI

20

Made by cutting TOPO NsiI-malE (1-28)::FXa::PstI, SalI, XbaI::FLAG-NheI
insertion with NsiI & NheI and cloning into pMPX-71 cut with PstI & XbaI.

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SEQ ID NO.: 268

pMPX-88 Male (1-28) fusion vector

5

SD old PstI +1

AGGAGGTTCTGCATATGAAAAT

1

M K I

10

AAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCC
GCCTC

4 K T G A R I L A L S A L T T M M F S A S

15

Factor Xa PstI SalI XbaI

GGCTCTCGCCAAAATCATCGAAGCCCGCCTGCAGGCCTCGGTCGACGCCGAATCT
AGAGA

20

24 A L A K I I E A R L Q A S V D A E S R D

FLAG

lost XbaI

TTATAAAGATGACGATGACAAATAATAAGCTAGAGGTACC
(transcriptional stop)

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PCT/US02/16877

44 Y K D D D D K

5 pMPX-84::male(1-28)::FXa::PstI, SalI, XbaI::FLAG

Temperature inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-male (1-28)::FXa::PstI, SalI, XbaI::FLAG-NheI
insertion with NsiI & NheI and cloning into pMPX-84 cut with PstI & XbaI.

10

SEQ ID NO.: 269

15 pMPX-93 Male (1-28) fusion vector

SD old PstI +1

AGGAGGTTCTGCATATGAAAAT

20

1

M K I

PCT/US02/16877

4 K T G A R I L A L S A L T T M M F S A S

Factor Xa	PstI	SalI	XbaI
+	+	+	+
+	+	+	-
+	+	-	+
+	-	+	+
+	-	-	+
+	-	+	-
+	-	-	-
-	+	+	+
-	+	+	-
-	+	-	+
-	+	-	-
-	-	+	+
-	-	+	-
-	-	-	+
-	-	-	-

10 24 A L A K I I E A R L Q A S V D A E S R D

FLAG lost XbaI

15 44 Y K D D D D K

pMPX-86::malE(1-28)::FXa::PstI, SalI, XbaI::FLAG

Temperature inducible, clone into PstI, SalI, XbaI

20 Made by cutting TOPO NsiI-malE (1-28)::FXa::PstI, SalI, XbaI::FLAG-NheI
insertion with NsiI & NheI and cloning into pMPX-86 cut with PstI & XbaI.

SEQ ID NO.: 270

PCT/US02/16877

SD old PstI +1

1 M K I

4 K T G A R I L A L S A L T T M M F S A S

24 A L A K I E E G K L V I W I N G D K G Y

44 N G L A E V G K K F E K D T G I K V T V

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2641

TGAGCATCCGGATAAACTGGAAGAGAAATTCCCACAGGTTGCGGCAACTGGCGAT
GGCCC

64 E H P D K L E E K F P Q V A A T G D G P

5

2701

TGACATTATCTTCTGGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGT
TGGC

84 D I I F W A H D R F G G Y A Q S G L L A

10

2761

TGAAATCACCCCGGACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGGGAT
GCCGT

104 E I T P D K A F Q D K L Y P F T W D A V

15

2821

ACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGA
TTTA

124 R Y N G K L I A Y P I A V E A L S L I Y

20

2881

TAACAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCGCTG
GATAA

144 N K D L L P N P P K T W E E I P A L D K

25

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2941

AGAACTGAAAGCGAAAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTAC
TTCAC

164 E L K A K G K S A L M F N L Q E P Y F T

5

3001

CTGGCCGCTGATTGCTGCTGACGGGGGTTATGCGTTCAAGTATGAAAACGGCAAG
TACGA

184 W P L I A A D G G Y A F K Y E N G K Y D

10

3061

CATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCCTG
GTTGA

204 I K D V G V D N A G A K A G L T F L V D

15

3121

CCTGATTAAAAACAAACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCT
GCCTT

224 L I K N K H M N A D T D Y S I A E A A F

20

3181

TAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATC
GACAC

244 N K G E T A M T I N G P W A W S N I D T

25

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3241

CAGCAAAGTGAATTATGGTGTAACGGTACTGCCGACCTTCAAGGGTCAACCATCC
AAACC

264 S K V N Y G V T V L P T F K G Q P S K P

5

3301

GTTCGTTGGCGTGCTGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGCTG
GCGAA

284 F V G V L S A G I N A A S P N K E L A K

10

3361

AGAGTTCCTCGAAAACCTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAA
GACAA

304 E F L E N Y L L T D E G L E A V N K D K

15

3421

ACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCA
CGTAT

324 P L G A V A L K S Y E E E L A K D P R I

20

pMPX-72::male(1-370 del 354-364)::FXa::PstI, SalI, XbaI::FLAG

Rhamnose inducible, clone into PstI, SalI, XbaI

25 Made by cutting TOPO NsiI-male (1-370 del 354-364)::FXa::PstI, SalI,
XbaI::FLAG-NheI insertion with NsiI & NheI and cloning into pMPX-72 cut with PstI &
XbaI.

WO 03/072014

PCT/US02/16877

SEQ ID NO.: 271

5 pMPX-76 MalE (1-370 del 354-364) fusion vector

SD old PstI +1

1621

CCATACCCGTTTTTTTTGGGCTAGCAGGAGGCCCTGCATATGAAAATAAAAACAGG
10 TGCAC

1

M K I K T G A

1681

GCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTCGGCTCTCGCC
15 AAAA

8

R I L A L S A L T T M M F S A S A L A K

1741

TCGAAGAAGGTAAACTGGTAATCTGGATTAACGGCGATAAAGGCTATAACGGTCT
20 CGCTG

28

I E E G K L V I W I N G D K G Y N G L A

1801

AAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAAGTCACCGTTGAGCATCC
25 GGATA

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PCT/US02/16877

48 E V G K K F E K D T G I K V T V E H P D

1861

AACTGGAAGAGAAATTCCCACAGGTTGCGGCAACTGGCGATGGCCCTGACATTAT
5 CTTCT

68 K L E E K F P Q V A A T G D G P D I I F

1921

GGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGCTGAAATCAC
10 CCCGG

88 W A H D R F G G Y A Q S G L L A E I T P

1981

ACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGGGATGCCGTACGTTACAA
15 CGGCA

108 D K A F Q D K L Y P F T W D A V R Y N G

2041

AGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGATTTATAACAAAGAT
20 CTGC

128 K L I A Y P I A V E A L S L I Y N K D L

2101

TGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCGCTGGATAAAGAACTGA
25 AAGCGA

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148 L P N P P K T W E E I P A L D K E L K A

2161

AAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTACTTCACCTGGCCGCT
5 GATTG

168 K G K S A L M F N L Q E P Y F T W P L I

2221

CTGCTGACGGGGTTATGCGTTCAAGTATGAAAACGGCAAGTACGACATTAAAGA
10 CGTGG

188 A A D G G Y A F K Y E N G K Y D I K D V

2281

GCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCCTGGTTGACCTGATTAA
15 AAACA

208 G V D N A G A K A G L T F L V D L I K N

2341

AACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCTGCCTTTAATAAAGG
20 CGAAA

228 K H M N A D T D Y S I A E A A F N K G E

2401

CAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATCGACACCAGCAAAGT
25 GAATT

PCT/US02/16877

2461

268 Y G V T V L P T F K G Q P S K P F V G V

10 TGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGCTGGCGAAAGAGTTCCT
CGAAA

288 L S A G I N A A S P N K E L A K E F L E

ACTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAAGACAAACCGCTGGG
15 TGCCG

308 N Y L L T D E G L E A V N K D K P L G A

20 TAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCACGTATTGCCGCCAC
CATGG

328 VALKSYEEELAKDPRIATM

161/268

WO 03/072014

PCT/US02/16877

2701

AAAACGCCCGAGTCCGCTTTCTGGTATGCCGTGCGTATCGAAGCCCGCCTGCAGGC
CTCGG

348 E N A Q S A F W Y A V R I E A R L Q A S

5

Sall XbaI FLAG Lost XbaI

2761

TCGACGCCGAATCTAGAGATTATAAAGATGACGATGACAAATAATAAGCTAGAGG
A(trxn stop)

10 368 V D A E S R D Y K D D D D K

pMPX-71::malE(1-370 del 354-364)::FXa::PstI, Sall, XbaI::FLAG

Arabinose inducible, clone into PstI, Sall, XbaI

15 Made by cutting TOPO NsiI-malE (1-370 del 354-364)::FXa::PstI, Sall,
XbaI::FLAG-NheI insertion with NsiI & NheI and cloning into pMPX-71 cut with PstI &
XbaI.

20

SEQ ID NO.: 272

pMPX-89 MalE (1-370 del 354-364) fusion vector

WO 03/072014

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SD old PstI +1

AGGAGGTTCTGCATATGAAAATAAAAACAGGTGCAC

1 M K I K T G A

5

GCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTCGGCTCTCGCC
AAAA

8 R I L A L S A L T T M M F S A S A L A K

10

TCGAAGAAGGTAAACTGGTAATCTGGATTAACGGCGATAAAGGCTATAACGGTCT
CGCTG

28 I E E G K L V I W I N G D K G Y N G L A

15

AAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAAGTCACCGTTGAGCATCC
GGATA

48 E V G K K F E K D T G I K V T V E H P D

20

AACTGGAAGAGAAATTCACACAGGTTGCGGCAACTGGCGATGGCCCTGACATTAT
CTTCT

68 K L E E K F P Q V A A T G D G P D I I F

25

WO 03/072014

PCT/US02/16877

GGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGCTGAAATCAC
CCCGG

88 W A H D R F G G Y A Q S G L L A E I T P

5

ACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGGGATGCCGTACGTTACAA
CGGCA

108 D K A F Q D K L Y P F T W D A V R Y N G

10

AGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGATTTATAACAAAGAT
CTGC

128 K L I A Y P I A V E A L S L I Y N K D L

15

TGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCGCTGGATAAAGAACTGA
AAGCGA

148 L P N P P K T W E E I P A L D K E L K A

20

AAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTACTTCACCTGGCCGCT
GATTG

168 K G K S A L M F N L Q E P Y F T W P L I

25

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PCT/US02/16877

CTGCTGACGGGGGTTATGCGTTCAAGTATGAAAACGGCAAGTACGACATTAAAGA
CGTGG

188 A A D G G Y A F K Y E N G K Y D I K D V

5

GCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCCTGGTTGACCTGATTAA
AAACA

208 G V D N A G A K A G L T F L V D L I K N

10

AACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCTGCCTTTAATAAAGG
CGAAA

228 K H M N A D T D Y S I A E A A F N K G E

15

CAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATCGACACCAGCAAAGT
GAATT

248 T A M T I N G P W A W S N I D T S K V N

20

ATGGTGTAACGGTACTGCCGACCTTCAAGGGTCAACCATCCAAACCGTTCGTTGG
CGTGC

268 Y G V T V L P T F K G Q P S K P F V G V

25

PCT/US02/16877

288 L S A G I N A A S P N K E L A K E F L E

308 N Y L L T D E G L E A V N K D K P L G A

328 VALKS YEEELAKDPRI AATM

20 348 E N A Q S A F W Y A V R I E A R L Q A S

166/268

WO 03/072014

PCT/US02/16877

368 V D A E S R D Y K D D D D K

pMPX-84::malE(1-370 del 354-364)::FXa::PstI, SalI, XbaI::FLAG

Temperature inducible, clone into PstI, SalI, XbaI

5

Made by cutting TOPO NsiI-malE (1-370 del 354-364)::FXa::PstI, SalI,
XbaI::FLAG-NheI insertion with NsiI & NheI and cloning into pMPX-84 cut with PstI &
XbaI.

10

SEQ ID NO.: 273

pMPX-94 MalE (1-370 del 354-364) fusion vector

15

SD old PstI +1

AGGAGGTTCTGCATATGAAAATAAAAACAGGTGCAC

1

M K I K T G A

20

GCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTCGGCTCTCGCC
AAAA

8

R I L A L S A L T T M M F S A S A L A K

PCT/US02/16877

28 I E E G K L V I W I N G D K G Y N G L A

48 E V G K K F E K D T G I K V T V E H P D

68 K L E E K F P Q V A A T G D G P D I I F

88 W A H D R F G G Y A Q S G L L A E I T P

108 D K A F Q D K L Y P F T W D A V R Y N G

168/268

PCT/US02/16877

5

10

AAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTACTTCACCTGGCCGCT
GATTG

15

20

GCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCCTGGTTGACCTGATTAA
AAACA

25

PCT/US02/16877

5

10

15

20

25

308 N Y L L T D E G L E A V N K D K P L G A

WO 03/072014

PCT/US02/16877

TAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCACGTATTGCCGCCAC
CATGG

328 V A L K S Y E E E L A K D P R I A A T M

5

Factor Xa PstI

AAAACGCCCAGTCCGCTTTCTGGTATGCCGTGCGTATCGAAGCCCGCCTGCAGGC
CTCGG

10 348 E N A Q S A F W Y A V R I E A R L Q A S

Sall XbaI FLAG Lost XbaI

TCGACGCCGAATCTAGAGATTATAAAGATGACGATGACAAATAATAAGCTAGAGG
15 (trxn stop)

368 V D A E S R D Y K D D D D K

pMPX-86::malE(1-370 del 354-364)::FXa::PstI, Sall, XbaI::FLAG

20 Temperature inducible, clone into PstI, Sall, XbaI

Made by cutting TOPO NsiI-malE (1-370 del 354-364)::FXa::PstI, Sall,
XbaI::FLAG-NheI insertion with NsiI & NheI and cloning into pMPX-86 cut with PstI &
XbaI.

25

WO 03/072014

PCT/US02/16877

SEQ ID NO.: 274

pMPX-79 TrxA (2-109 del 103-107) fusion vector

5

SD PstI SalI XbaI +2 trxA(del 103-107)

1

TAGCAGGAGGCCCTGCAGGCCTCGGTCGACGCCGAATCTAGAAGCGATAAAATTA
TT

10

1

A S V D A E S R S D K I I

61

CACCTGACTGACGACAGTTTTGACACGGATGTACTCAAAGCGGACGGGGCGATCC
TCGTC

15

17

H L T D D S F D T D V L K A D G A I L V

121

GATTTCTGGGCAGAGTGGTGCGGTCCGTGCAAAATGATCGCCCCGATTCTGGATG
AAATC

20

37

D F W A E W C G P C K M I A P I L D E I

181

GCTGACGAATATCAGGGCAAACCTGACCGTTGCAAACTGAACATCGATCAAAACC
CTGGC

25

57

A D E Y Q G K L T V A K L N I D Q N P G

PCT/US02/16877

ACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTGCTGTTCAAAAACG
GTGAA

5

GTGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTGAAAGAGAACCTGG
CGGAT

10

Lost XbaI

15

117

pMPX-71::PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG

Arabinose inducible, clone into PstI, SalI, XbaI

20

Made by cutting TOPO PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG-NheI insertion with PstI & NheI and cloning into pMPX-71 cut with PstI & XbaI.

WO 03/072014

PCT/US02/16877

SEQ ID NO.: 275

5 pMPX-78 TrxA (2-109 del 103-107) fusion vector

SD PstI

1
GAATTCAGGCGCTTTT TAGACTGGTCGTAATGAAATTCAGGAGGTTCTGCAGGCCT
10 C

1 A S

Sall XbaI +2 trxA(del 103-107)

61
15 GGTCGACGCCGAATCTAGAAGCGATAAAATTATTCACCTGACTGACGACAGTTTT
GACAC

6 V D A E S R S D K I I H L T D D S F D T

121
20 GGATGTACTCAAAGCGGACGGGGCGATCCTCGTCGATTTCTGGGCAGAGTGGTGC
GGTCC

26 D V L K A D G A I L V D F W A E W C G P

WO 03/072014

PCT/US02/16877

181

GTGCAAAATGATCGCCCCGATTCTGGATGAAATCGCTGACGAATATCAGGGCAAA
CTGAC

46 C K M I A P I L D E I A D E Y Q G K L T

5

241

CGTTGCAAAACTGAACATCGATCAAAACCCTGGCACTGCGCCGAAATATGGCATC
CGTGG

66 V A K L N I D Q N P G T A P K Y G I R G

10

301

TATCCCGACTCTGCTGCTGTTCAAAAACGGTGAAGTGGCGGCAACCAAAGTGGGT
GCACT

86 I P T L L L F K N G E V A A T K V G A L

15

FLAG

361

GTCTAAAGGTCAGTTGAAAGAGAACCTGGCGGATTATAAAGATGACGATGACAAA
TAATAA

20

106 S K G Q L K E N L A D Y K D D D D K

lost XbaI

GCTAGAGG (transcriptional stop)

25

pMPX-72::PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG

WO 03/072014

PCT/US02/16877

Rhamnose inducible, clone into PstI, SalI, XbaI

+1 Met required for protein to be fused

Made by cutting TOPO PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG-NheI
5 insertion with PstI & NheI and cloning into pMPX-72 cut with PstI & XbaI.

SEQ ID NO.: 276

10

pMPX-90 TrxA (2-109 del 103-107) fusion vector

SD PstI SalI XbaI +2 trxA(del 103-107)

15 AGGAGGTTCTGCAGGCCTCGGTCGACGCCGAATCTAGAAGCGATAAAATTATT

1 A S V D A E S R S D K I I

CACCTGACTGACGACAGTTTTGACACGGATGTACTCAAAGCGGACGGGGCGATCC
20 TCGTC

17 H L T D D S F D T D V L K A D G A I L V

WO 03/072014

PCT/US02/16877

GATTTCTGGGCAGAGTGGTGCGGTCCGTGCAAAATGATCGCCCCGATTCTGGATG
AAATC

37 D F W A E W C G P C K M I A P I L D E I

5

GCTGACGAATATCAGGGCAAACCTGACCGTTGCAAAACTGAACATCGATCAAAACC
CTGGC

57 A D E Y Q G K L T V A K L N I D Q N P G

10

ACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTGCTGTTCAAAAACG
GTGAA

77 T A P K Y G I R G I P T L L L F K N G E

15

GTGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTGAAAGAGAACCTGG
CGGAT

97 V A A T K V G A L S K G Q L K E N L A D

20

FLAG

Lost XbaI

TATAAAGATGACGATGACAAATAATAAGCTAGAGGTACC

(transcriptional stop)

117 Y K D D D D K

25

WO 03/072014

PCT/US02/16877

pMPX-84::PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG

Temperature inducible, clone into PstI, SalI, XbaI

+1 Met required for protein to be fused

- 5 Made by cutting TOPO PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG-NheI
insertion with PstI & NheI and cloning into pMPX-84 cut with PstI & XbaI.

SEQ ID NO.: 277

10

pMPX-95 TrxA (2-109 del 103-107) fusion vector

SD PstI SalI XbaI +2 trxA(del 103-107)

15 AGGAGGTTCTGCAGGCCTCGGTTCGACGCCGAATCTAGAAGCGATAAAATTATT

1 A S V D A E S R S D K I I

 CACCTGACTGACGACAGTTTTGACACGGATGTACTCAAAGCGGACGGGGCGATCC
20 TCGTC

17 H L T D D S F D T D V L K A D G A I L V

PCT/US02/16877

5

10

15

ACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTGCTGTTCAAAAACG
GTGAA

77 T A P K Y G I R G I P T L L L F K N G E

GTGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTGAAAGAGAACCTGG
CGGAT

97 V A A T K V G A L S K G Q L K E N L A D

20

FLAG

Lost XbaI

TATAAAGATGACGATGACAAATAATAAGCTAGAGGTACC

(transcriptional stop)

117 Y K D D D D K

25

WO 03/072014

PCT/US02/16877

pMPX-86::PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG

Temperature inducible, clone into PstI, SalI, XbaI.

+1 Met required for protein to be fused

- 5 Made by cutting TOPO PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG-NheI
insertion with PstI & NheI and cloning into pMPX-86 cut with PstI & XbaI.

SEQ ID NO.: 278

10

pMPX-80 MalE (1-28) MCS TrxA (2-109 del 103-107) fusion vector

SD Lost PstI +1

malE(1-28)

15

2401

GAATTCAGGCGCTTTT TAGACTGGTCGTAATGAAATTCAGGAGGTTCTGCATATGA
AAAT

1

M K I

20

2461

AAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCC
GCCTC

4

K T G A R I L A L S A L T T M M F S A S

WO 03/072014

PCT/US02/16877

Factor Xa PstI SalI XbaI

2521

GGCTCTCGCCAAAATCATCGAAGCCCGCCTGCAGGCCTCGGTCTGACGCCGAATCT
AGAAG

5 24 A L A K I I E A R L Q A S V D A E S R S

+2 trxA (2-109 del 103-107)

2581

CGATAAAATTATTACCTGACTGACGACAGTTTTTGACACGGATGTACTCAAAGCG
10 GACGG

44 D K I I H L T D D S F D T D V L K A D G

2641

GGCGATCCTCGTCGATTTCTGGGCAGAGTGGTGCGGTCCGTGCAAAATGATCGCC
15 CCGAT

64 A I L V D F W A E W C G P C K M I A P I

2701

TCTGGATGAAATCGCTGACGAATATCAGGGCAAAGTACCGTTGCAAAAGTGAAC
20 ATCGA

84 L D E I A D E Y Q G K L T V A K L N I D

2761

TCAAAACCCTGGCACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTG
25 CTGTT

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104 Q N P G T A P K Y G I R G I P T L L L F

2821

CAAAAACGGTGAAGTGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTG
5 AAAGA

124 K N G E V A A T K V G A L S K G Q L K E

FLAG

Lost XbaI

2881

10 GAACCTGGCGGATTATAAAGATGACGATGACAAATAATAAGCTAGAGG (trxn stop)

144 N L A D Y K D D D D K

pMPX-72::malE(1-28)::FXa::PstI, SalI, XbaI::TrxA(1-109 del 103-107)::FLAG

Rhamnose inducible, clone into PstI, SalI, XbaI

15

Made by cutting TOPO NsiI-malE (1-28)::FXa::PstI, SalI, XbaI::FLAG-NheI
insertion with NsiI & XbaI and cloning into pMPX-78 cut with PstI & XbaI.

SEQ ID NO.: 279

20

pMPX-81 MalE (1-28) MCS TrxA (2-109 del 103-107) fusion vector

SD Lost PstI +1 malE (1-28)

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1621

CCATACCCGTTTTTTTTGGGCTAGCAGGAGGCCCTGCATATGAAAATAAAAACAGG
TGCAC

1

M K I K T G A

5

1681

GCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTCGGCTCTCGCC
AAAA

8

R I L A L S A L T T M M F S A S A L A K

10

+2 trxA(2-109 del
103-107)

Factor Xa PstI

SalI

XbaI

1741

TCATCGAAGCCCGCCTGCAGGCCTCGGTCGACGCCGAATCTAGAAGCGATAAAAT
15 TATTC

28

I I E A R L Q A S V D A E S R S D K I I

1801

ACCTGACTGACGACAGTTTTGACACGGATGTACTCAAAGCGGACGGGGCGATCCT
20 CGTCG

48

H L T D D S F D T D V L K A D G A I L V

1861

ATTTCTGGGCAGAGTGGTGCGGTCCGTGCAAAATGATCGCCCCGATTCTGGATGA
25 AATCG

68

D F W A E W C G P C K M I A P I L D E I

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1921

CTGACGAATATCAGGGCAAACCTGACCGTTGCAAAACTGAACATCGATCAAAACCC
TGGCA

5 88 A D E Y Q G K L T V A K L N I D Q N P G

1981

CTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTGCTGTTCAAAAACGGT
GAAG

10 108 T A P K Y G I R G I P T L L L F K N G E

2041

TGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTGAAAGAGAACCTGGC
GGATT

15 128 V A A T K V G A L S K G Q L K E N L A D

FLAG

2101 ATAAAGATGACGATGACAAATAATAAGCTAGAGG (transcriptional
stop)

20 148 Y K D D D D K

pMPX-71::malE(1-28)::FXa::PstI, SalI, XbaI::TrxA(1-109 del 103-107)::FLAG

Arabinose inducible, clone into PstI, SalI, XbaI

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Made by cutting TOPO NsiI-malE (1-28)::FXa::PstI, SalI, XbaI::FLAG-NheI
insertion with NsiI & XbaI and cloning into pMPX-79 cut with PstI & XbaI.

5 SEQ ID NO.: 280

pMPX-91 MalE (1-28) MCS TrxA (2-109 del 103-107) fusion vector

SD Lost PstI +1

10 malE(1-28)

AGGAGGTTCTGCATATGAAAAT

1

M K I

15

AAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCC
GCCTC

4

K T G A R I L A L S A L T T M M F S A S

20

Factor Xa PstI SalI XbaI

GGCTCTCGCCAAAATCATCGAAGCCCGCCTGCAGGCCTCGGTCTGACGCCGAATCT
AGAAG

24

A L A K I I E A R L Q A S V D A E S R S

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+2 trxA (2-109 del 103-107)

CGATAAAATTATTACCTGACTGACGACAGTTTTGACACGGATGTACTCAAAGCG
5 GACGG

44 D K I I H L T D D S F D T D V L K A D G

GGCGATCCTCGTCGATTTCTGGGCAGAGTGGTGCGGTCCGTGCAAAATGATCGCC
10 CCGAT

64 A I L V D F W A E W C G P C K M I A P I

TCTGGATGAAATCGCTGACGAATATCAGGGCAAACCTGACCGTTGCAAAACTGAAC
15 ATCGA

84 L D E I A D E Y Q G K L T V A K L N I D

TCAAAACCCTGGCACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTG
20 CTGTT

104 Q N P G T A P K Y G I R G I P T L L L F

CAAAAACGGTGAAGTGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTG
25 AAAGA

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124 K N G E V A A T K V G A L S K G Q L K E

FLAG

Lost XbaI

5 GAACCTGGCGGATTATAAAGATGACGATGACAAATAATAAGCTAGAGGTACC
(trxn stop)

144 N L A D Y K D D D D K

pMPX-84::malE(1-28)::FXa::PstI, SalI, XbaI::TrxA(1-109 del 103-107)::FLAG

10 Temperature inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-malE (1-28)::FXa::PstI, SalI, XbaI::FLAG-NheI
insertion with NsiI & XbaI and cloning into pMPX-90 cut with PstI & XbaI.

15

SEQ ID NO.: 281

pMPX-96 MalE (1-28) MCS TrxA (2-109 del 103-107) fusion vector

20

SD Lost PstI +1

malE(1-28)

AGGAGGTTCTGCATATGAAAAT

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PCT/US02/16877

1

M K I

AAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCC
5 GCCTC

4 K T G A R I L A L S A L T T M M F S A S

Factor Xa PstI SalI XbaI

10 GGCTCTCGCCAAAATCATCGAAGCCCGCCTGCAGGCCTCGGTCGACGCCGAATCT
AGAAG

24 A L A K I I E A R L Q A S V D A E S R S

+2 trxA (2-109 del 103-107)

15

CGATAAAATTATTACCTGACTGACGACAGTTTTGACACGGATGTACTCAAAGCG
GACGG

44 D K I I H L T D D S F D T D V L K A D G

20

GGCGATCCTCGTCGATTTCTGGGCAGAGTGGTGCGGTCCGTGCAAAATGATCGCC
CCGAT

64 A I L V D F W A E W C G P C K M I A P I

WO 03/072014

PCT/US02/16877

TCTGGATGAAATCGCTGACGAATATCAGGGCAAACCTGACCGTTGCAAAACTGAAC
ATCGA

84 L D E I A D E Y Q G K L T V A K L N I D

5

TCAAAACCCTGGCACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTG
CTGTT

104 Q N P G T A P K Y G I R G I P T L L L F

10

CAAAAACGGTGAAGTGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTG
AAAGA

124 K N G E V A A T K V G A L S K G Q L K E

15

FLAG

Lost XbaI

GAACCTGGCGGATTATAAAGATGACGATGACAAATAATAAGCTAGAGGTACC
(txn stop)

20

144 N L A D Y K D D D D K

pMPX-86::malE(1-28)::FXa::PstI, SalI, XbaI::TrxA(1-109 del 103-107)::FLAG

Temperature inducible, clone into PstI, SalI, XbaI

WO 03/072014

PCT/US02/16877

Made by cutting TOPO NsiI-malE (1-28)::FXa::PstI, SalI, XbaI::FLAG-NheI
insertion with NsiI & XbaI and cloning into pMPX-95 cut with PstI & XbaI.

5 SEQ ID NO.: 282

pMPX-83 MalE (1-370 del 354-364) MCS TrxA (2-109 del 103-107) fusion vector

SD Lost PstI +1

10 malE(1-28)

2401

GAATTCAGGCGCTTTT TAGACTGGTCGTAATGAAATTCAGGAGGTTCTGCATATGA
AAAT

1

M K I

15

2461

AAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCC
GCCTC

4

K T G A R I L A L S A L T T M M F S A S

20

2521

GGCTCTCGCCAAAATCGAAGAAGGTAAACTGGTAATCTGGATTAACGGCGATAAA
GGCTA

24

A L A K I E E G K L V I W I N G D K G Y

25

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PCT/US02/16877

2581

TAACGGTCTCGCTGAAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAAGTC
ACCGT

44 N G L A E V G K K F E K D T G I K V T V

5

2641

TGAGCATCCGGATAAACTGGAAGAGAAATTCCCACAGGTTGCGGCAACTGGCGAT
GGCCC

64 E H P D K L E E K F P Q V A A T G D G P

10

2701

TGACATTATCTTCTGGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGT
TGGC

84 D I I F W A H D R F G G Y A Q S G L L A

15

2761

TGAAATCACCCCGGACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGGGAT
GCCGT

104 E I T P D K A F Q D K L Y P F T W D A V

20

2821

ACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGA
TTTA

124 R Y N G K L I A Y P I A V E A L S L I Y

25

WO 03/072014

PCT/US02/16877

2881

TAACAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCGCTG
GATAA

144 N K D L L P N P P K T W E E I P A L D K

5

2941

AGAACTGAAAGCGAAAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTAC
TTCAC

164 E L K A K G K S A L M F N L Q E P Y F T

10

3001

CTGGCCGCTGATTGCTGCTGACGGGGGTTATGCGTTCAAGTATGAAAACGGCAAG
TACGA

184 W P L I A A D G G Y A F K Y E N G K Y D

15

3061

CATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCCTG
GTTGA

204 I K D V G V D N A G A K A G L T F L V D

20

3121

CCTGATTAAAAACAAACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCT
GCCTT

224 L I K N K H M N A D T D Y S I A E A A F

25

WO 03/072014

PCT/US02/16877

3181

TAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATC
GACAC

244 N K G E T A M T I N G P W A W S N I D T

5

3241

CAGCAAAGTGAATTATGGTGTAACGGTACTGCCGACCTTCAAGGGTCAACCATCC
AAACC

264 S K V N Y G V T V L P T F K G Q P S K P

10

3301

GTTCGTTGGCGTGCTGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGCTG
GCGAA

284 F V G V L S A G I N A A S P N K E L A K

15

3361

AGAGTTCCTCGAAAACCTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAA
GACAA

304 E F L E N Y L L T D E G L E A V N K D K

20

3421

ACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCA
CGTAT

324 P L G A V A L K S Y E E E L A K D P R I

25

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Factor Xa

3481

5 TGCCGCCACCATGGAAAACGCCCAGTCCGCTTTCTGGTATGCCGTGCGTATCGAA
GCCCCG

344 A A T M E N A Q S A F W Y A V R I E A R

PstI

SalI

XbaI +2 trxA (2-109 del 103-107)

3541

10 CCTGCAGGCCTCGGTTCGACGCCGAATCTAGAAGCGATAAAAATTATTCACCTGACT
GACGA

364 L Q A S V D A E S R S D K I I H L T D D

3601

15 CAGTTTTGACACGGATGTACTCAAAGCGGACGGGGCGATCCTCGTCGATTTCTGG
GCAGA

384 S F D T D V L K A D G A I L V D F W A E

3661

20 GTGGTGCGGTCCGTGCAAAAATGATCGCCCCGATTCTGGATGAAATCGCTGACGAA
TATCA

404 W C G P C K M I A P I L D E I A D E Y Q

3721

25 GGGCAAACCTGACCGTTGCAAACTGAACATCGATCAAAACCCTGGCACTGCGCCG
AAATA

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424 G K L T V A K L N I D Q N P G T A P K Y

3781

TGGCATCCGTGGTATCCCGACTCTGCTGCTGTTCAAAAACGGTGAAGTGGCGGCA
5 ACCAA

444 G I R G I P T L L L F K N G E V A A T K

FLAG

10 3841
AGTGGGTGCACTGTCTAAAGGTCAGTTGAAAGAGAACCTGGCGGATTATAAAGAT
GACGA

464 V G A L S K G Q L K E N L A D Y K D D D

15 3901 TGACAAATAATAAGCTAGAGG (transcriptional stop)

484 D K

pMPX-72::malE(1-320 del 354-364)::FXa::PstI, SalI, XbaI::TrxA(1-109 del 103-
107)::FLAG.

20 Rhamnose inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-malE (1-370 del 354-364)::FXa::PstI, SalI,
XbaI::FLAG-NheI insertion with NsiI & XbaI and cloning into pMPX-78 cut with PstI &
XbaI.

25

WO 03/072014

PCT/US02/16877

SEQ ID NO.: 283

pMPX-82 MalE (1-370 del 354-364) MCS TrxA (2-109 del 103-107) fusion vector

5

SD Lost PstI +1 malE (1-370 del
352-362)

1621

CCATACCCGTTTTTTTGGGCTAGCAGGAGGCCCTGCATATGAAAATAAAAAACAGG
10 TGCAC

1

M K I K T G A

1681

GCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTCGGCTCTCGCC
15 AAAA

8

R I L A L S A L T T M M F S A S A L A K

1741

TCGAAGAAGGTAAACTGGTAATCTGGATTAACGGCGATAAAGGCTATAACGGTCT
20 CGCTG

28

I E E G K L V I W I N G D K G Y N G L A

1801

AAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAAGTCACCGTTGAGCATCC
25 GGATA

WO 03/072014

PCT/US02/16877

48 E V G K K F E K D T G I K V T V E H P D

1861

AACTGGAAGAGAAATTCCCACAGGTTGCGGCAACTGGCGATGGCCCTGACATTAT
5 CTTCT

68 K L E E K F P Q V A A T G D G P D I I F

1921

GGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGCTGAAATCAC
10 CCCGG

88 W A H D R F G G Y A Q S G L L A E I T P

1981

ACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGGGATGCCGTACGTTACAA
15 CGGCA

108 D K A F Q D K L Y P F T W D A V R Y N G

2041

AGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGATTTATAACAAAGAT
20 CTGC

128 K L I A Y P I A V E A L S L I Y N K D L

2101

TGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCGCTGGATAAAGAACTGA
25 AAGCGA

WO 03/072014

PCT/US02/16877

148 L P N P P K T W E E I P A L D K E L K A

2161

AAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTACTTCACCTGGCCGCT
5 GATTG

168 K G K S A L M F N L Q E P Y F T W P L I

2221

CTGCTGACGGGGGTTATGCGTTCAAGTATGAAAACGGCAAGTACGACATTAAAGA
10 CGTGG

188 A A D G G Y A F K Y E N G K Y D I K D V

2281

GCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCCTGGTTGACCTGATTAA
15 AAACA

208 G V D N A G A K A G L T F L V D L I K N

2341

AACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCTGCCTTTAATAAAGG
20 CGAAA

228 K H M N A D T D Y S I A E A A F N K G E

2401

CAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATCGACACCAGCAAAGT
25 GAATT

WO 03/072014

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248 T A M T I N G P W A W S N I D T S K V N

2461

ATGGTGTAACGGTACTGCCGACCTTCAAGGGTCAACCATCCAAACCGTTCGTTGG

5 CGTGC

268 Y G V T V L P T F K G Q P S K P F V G V

2521

TGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGCTGGCGAAAGAGTTCCT

10 CGAAA

288 L S A G I N A A S P N K E L A K E F L E

2581

ACTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAAGACAAACCGCTGGG

15 TGCCG

308 N Y L L T D E G L E A V N K D K P L G A

2641

TAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCACGTATTGCCGCCAC

20 CATGG

328 V A L K S Y E E E L A K D P R I A A T M

Factor Xa PstI

WO 03/072014

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2701

AAAACGCCCAGTCCGCTTTCTGGTATGCCGTGCGTATCGAAGCCCGCCTGCAGGC
CTCGG

348 E N A Q S A F W Y A V R I E A R L Q A S

5

SalI XbaI +2 trxA (2-109 del 103-107)

2761

TCGACGCCGAATCTAGAAGCGATAAAATTATTCACCTGACTGACGACAGTTTTGA
CACGG

10 368 V D A E S R S D K I I H L T D D S F D T

2821

ATGTACTCAAAGCGGACGGGGCGATCCTCGTCGATTTCTGGGCAGAGTGGTGCGG
TCCGT

15 388 D V L K A D G A I L V D F W A E W C G P

2881

GCAAAATGATCGCCCCGATTCTGGATGAAATCGCTGACGAATATCAGGGCAAAC
TACCG

20 408 C K M I A P I L D E I A D E Y Q G K L T

2941

TTGCAAAACTGAACATCGATCAAAACCCTGGCACTGCGCCGAAATATGGCATCCG
TGGTA

25 428 V A K L N I D Q N P G T A P K Y G I R G

WO 03/072014

PCT/US02/16877

3001

TCCCGACTCTGCTGCTGTTCAAAAACGGTGAAGTGGCGGCAACCAAAGTGGGTGC
ACTGT

5 448 I P T L L L F K N G E V A A T K V G A L

FLAG

3061

CTAAAGGTCAGTTGAAAGAGAACCTGGCGGATTATAAAGATGACGATGACAAATA
10 ATAAG

468 S K G Q L K E N L A D Y K D D D D K

Lost XbaI

CTAGAGG (transcriptional stop)

15

pMPX-71::male(1-370 del 354-364)::FXa::PstI, SalI, XbaI::TrxA(1-109 del 103-
107)::FLAG

Arabinose inducible, clone into PstI, SalI, XbaI

20

Made by cutting TOPO NsiI-male (1-370 del 354-364)::FXa::PstI, SalI,
XbaI::FLAG-NheI insertion with NsiI & XbaI and cloning into pMPX-79 cut with PstI &
XbaI.

WO 03/072014

PCT/US02/16877

SEQ ID NO.: 284

pMPX-92 MalE (1-370 del 354-364)-MCS TrxA (2-109 del 103-107) fusion vector

5

SD Lost PstI +1 malE (1-370 del
354-364)

AGGAGGTTCTGCATATGAAAATAAAAACAGGTGCAC

10

1

M K I K T G A

GCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTCGGCTCTCGCC
AAAA

15

8

R I L A L S A L T T M M F S A S A L A K

TCGAAGAAGGTAAACTGGTAATCTGGATTAACGGCGATAAAGGCTATAACGGTCT
CGCTG

20

28

I E E G K L V I W I N G D K G Y N G L A

AAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAAGTCACCGTTGAGCATCC
GGATA

25

48

E V G K K F E K D T G I K V T V E H P D

WO 03/072014

PCT/US02/16877

AACTGGAAGAGAAATTCCCACAGGTTGCGGCAACTGGCGATGGCCCTGACATTAT
CTTCT

5 68 K L E E K F P Q V A A T G D G P D I I F

GGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGCTGAAATCAC
CCCGG

10 88 W A H D R F G G Y A Q S G L L A E I T P

ACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGGGATGCCGTACGTTACAA
CGGCA

15 108 D K A F Q D K L Y P F T W D A V R Y N G

AGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGATTTATAACAAAGAT
CTGC

20 128 K L I A Y P I A V E A L S L I Y N K D L

TGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCGCTGGATAAAGAACTGA
AAGCGA

25 148 L P N P P K T W E E I P A L D K E L K A

WO 03/072014

PCT/US02/16877

AAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTACTTCACCTGGCCGCT
GATTG

5 168 K G K S A L M F N L Q E P Y F T W P L I

CTGCTGACGGGGGTTATGCGTTCAAGTATGAAAACGGCAAGTACGACATTAAAGA
CGTGG

10 188 A A D G G Y A F K Y E N G K Y D I K D V

GCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCCTGGTTGACCTGATTAA
AAACA

15 208 G V D N A G A K A G L T F L V D L I K N

2341
AACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCTGCCTTTAATAAAGG
CGAAA

20 228 K H M N A D T D Y S I A E A A F N K G E

2401
CAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATCGACACCAGCAAAGT
GAATT

25 248 T A M T I N G P W A W S N I D T S K V N

WO 03/072014

PCT/US02/16877

2461

ATGGTGTAACGGTACTGCCGACCTTCAAGGGTCAACCATCCAAACCGTTCGTTGG
CGTGC

5 268 Y G V T V L P T F K G Q P S K P F V G V

2521

TGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGCTGGCGAAAGAGTTCCT
CGAAA

10 288 L S A G I N A A S P N K E L A K E F L E

2581

ACTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAAGACAAACCGCTGGG
TGCCG

15 308 N Y L L T D E G L E A V N K D K P L G A

2641

TAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCACGTATTGCCGCCAC
CATGG

20 328 V A L K S Y E E E L A K D P R I A A T M

Factor Xa PstI

2701

AAAACGCCCAGTCCGCTTTCTGGTATGCCGTGCGTATCGAAGCCCGCCTGCAGGC
25 CTCGG

WO 03/072014

PCT/US02/16877

348 E N A Q S A F W Y A V R I E A R L Q A S

SalI XbaI +2 trxA (2-109 del 103-107)

2761

5 TCGACGCCGAATCTAGAAGCGATAAAATTATTACCTGACTGACGACAGTTTGA
CACGG

368 V D A E S R S D K I I H L T D D S F D T

2821

10 ATGTACTCAAAGCGGACGGGGCGATCCTCGTCGATTTCTGGGCAGAGTGGTGCGG
TCCGT

388 D V L K A D G A I L V D F W A E W C G P

2881

15 GCAAAATGATCGCCCCGATTCTGGATGAAATCGCTGACGAATATCAGGGCAAAC
TACCG

408 C K M I A P I L D E I A D E Y Q G K L T

2941

20 TTGCAAAACTGAACATCGATCAAAACCCTGGCACTGCGCCGAAATATGGCATCCG
TGGTA

428 V A K L N I D Q N P G T A P K Y G I R G

PCT/US02/16877

TCCCGACTCTGCTGCTGTTCAAAAACGGTGAAGTGGCGGCAACCAAAGTGGGTGC
ACTGT

448 I P T L L L F K N G E V A A T K V G A L

5

FLAG

CTAAAGGTCAGTTGAAAAGAGAACCTGGCGGATTATAAAGATGACGATGACAAATA
ATAAG

10 468 S K G Q L K E N L A D Y K D D D D K

Lost XbaI

CTAGAGGTACC (transcriptional stop)

15 pMPX-84::malE(1-370 del 354-364)::FXa::PstI, SalI, XbaI::TrxA(1-109 del 103-107)::FLAG

Temperature inducible, clone into PstI, SalI, XbaI

20 Made by cutting TOPO NsiI-maleE (1-370 del 354-364)::FXa::PstI, SalI,
XbaI::FLAG-NheI insertion with NsiI & XbaI and cloning into pMPX-90 cut with PstI &
XbaI.

WO 03/072014

PCT/US02/16877

SEQ ID NO.: 285

pMPX-97 MalE (1-370 del 354-364) MCS TrxA (2-109 del 103-107) fusion vector

5 SD Lost PstI +1 malE (1-370 del
354-364)

AGGAGGTTCTGCATATGAAAATAAAAACAGGTGCAC

1 M K I K T G A

10

GCATCCTCGCATTATCCGCATTAAACGACGATGATGTTTTCCGCCTCGGCTCTCGCC
AAAA

8 R I L A L S A L T T M M F S A S A L A K

15

TCGAAGAAGGTAAACTGGTAATCTGGATTAACGGCGATAAAGGCTATAACGGTCT
CGCTG

28 I E E G K L V I W I N G D K G Y N G L A

20

AAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAAGTCACCGTTGAGCATCC
GGATA

48 E V G K K F E K D T G I K V T V E H P D

25

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5

10

ACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGGGATGCCGTACGTTACAA
CGGCA

15

AGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGATTTATAACAAAGAT
CTGC

20

TGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCCTGGATAAAGAAGCTGA
AAGCGA

25

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10

15

20

25

248 T A M T I N G P W A W S N I D T S K V N

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2461

ATGGTGTAACGGTACTGCCGACCTTCAAGGGTCAACCATCCAAACCGTTCGTTGG
CGTGC

268 Y G V T V L P T F K G Q P S K P F V G V

5

2521

TGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGCTGGCGAAAGAGTTCCT
CGAAA

288 L S A G I N A A S P N K E L A K E F L E

10

2581

ACTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAAGACAAACCGCTGGG
TGCCG

308 N Y L L T D E G L E A V N K D K P L G A

15

2641

TAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCACGTATTGCCGCCAC
CATGG

328 V A L K S Y E E E L A K D P R I A A T M

20

Factor Xa PstI

2701

AAAACGCCCAGTCCGCTTTCTGGTATGCCGTGCGTATCGAAGCCCGCCTGCAGGC
CTCGG

25

348 E N A Q S A F W Y A V R I E A R L Q A S

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SalI XbaI +2 trxA (2-109 del 103-107)

2761

TCGACGCCGAATCTAGAAGCGATAAAATTATTACCTGACTGACGACAGTTTGA
5 CACGG

368 V D A E S R S D K I I H L T D D S F D T

2821

ATGTACTCAAAGCGGACGGGGCGATCCTCGTCGATTTCTGGGCAGAGTGGTGCGG
10 TCCGT

388 D V L K A D G A I L V D F W A E W C G P

2881

GCAAAATGATCGCCCCGATTCTGGATGAAATCGCTGACGAATATCAGGGCAAAC
15 GACCG

408 C K M I A P I L D E I A D E Y Q G K L T

2941

TTGCAAAACTGAACATCGATCAAAACCCTGGCACTGCGCCGAAATATGGCATCCG
20 TGGTA

428 V A K L N I D Q N P G T A P K Y G I R G

3001

TCCCGACTCTGCTGCTGTTCAAAAACGGTGAAGTGGCGGCAACCAAAGTGGGTGC
25 ACTGT

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448 I P T L L L F K N G E V A A T K V G A L

FLAG

3061

5 CTAAAGGTCAGTTGAAAGAGAACCTGGCGGATTATAAAGATGACGATGACAAATA
ATAAG

468 S K G Q L K E N L A D Y K D D D D K

Lost XbaI

10 CTAGAGGTACC (transcriptional stop)

pMPX-86::malE(1-370 del 354-364)::FXa::PstI, SalI, XbaI::TrxA(1-109 del 103-107)::FLAG

Temperature inducible, clone into PstI, SalI, XbaI

15

Made by cutting TOPO NsiI-malE (1-370 del 354-364)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & XbaI and cloning into pMPX-95 cut with PstI & XbaI.

20

SEQ ID NO.: 151

pMPX-66 arabinose-inducible expression vector

25 1 TCGCGCGTTT CGGTGATGAC GGTGAAAACC TCTGACACAT GCAGCTCCCG
GAGACGGTCA
61 CAGCTTGTCT GTAAGCGGAT GCCGGGAGCA GACAAGCCCG TCAGGGCGCG
TCAGCGGGTG

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121 TTGGCGGGTG TCGGGGCTGG CTTAACTATG CGGCATCAGA GCAGATTGTA
CTGAGAGTGC
181 ACCATATGCG GTGTGAAATA CCGCACAGAT GCGTAAGGAG AAAATACCGC
ATCAGGCGCC
5 241 ATTCGCCATT CAGGCTGCGC AACTGTTGGG AAGGGCGATC GGTGCGGGCC
TCTTCGCTAT
301 TACGCCAGCT GCGGAAAGGG GGATGTGCTG CAAGGCGATT AAGTTGGGTA
ACGCCAGGGT

10
361 TTTCCAGTC ACGACGTTGT AAAACGACGG CCAGTGCCAA GCTTCAAGCC
GTCAATTGTC HindIII

15 421 TGATTCGTTA CCAATTAAGA CAACTTGACG GCTACATCAT TCACTTTTTTC
TTCACAACCG Stop araC

20 481 GCACGGAAC TCGTCGGGCT GGCCCCGGTG CATTTTTAA ATACCCGCGA
GAAATAGAGT
541 TGATCGTCAA AACCAACATT GCGACCGACG GTGGCGATAG GCATCCGGGT
GGTGCTCAAA
601 AGCAGCTTCG CCTGGCTGAT ACGTTGGTCC TCGCGCCAGC TTAAGACGCT
AATCCCTAAC

25 661 TGCTGGCGGA AAAGATGTGA CAGACGCGAC GGCGACAAGC AAACATGCTG
TGCGACGCTG
721 GCGATATCAA AATTGCTGTC TGCCAGGTGA TCGCTGATGT ACTGACAAGC
CTCGCGTACC

30 781 CGATTATCCA TCGGTGGATG GAGCGACTCG TTAATCGCTT CCATGCGCCG
CAGTAACAAT
841 TGCTCAAGCA GATTTATCGC CAGCAGCTCC GAATAGCGCC CTTCCCCTTG
CCCGGCGTTA

35 901 ATGATTTGCC CAAACAGGTC GCTGAAATGC GGCTGGTGCG CTTTCATCCG
GCGAAAGAAC
961 CCCGTATTGG CAAATATTGA CGGCCAGTTA AGCCATTCAT GCCAGTAGGC
GCGCGGACGA

40 1021 AAGTAAACCC ACTGGTGATA CCATTCGCGA GCCTCCGGAT GACGACCGTA
GTGATGAATC
1081 TCTCCTGGCG GGAACAGCAA AATATCACCC GGTGCGCAA CAAATTCTCG
TCCCTGATTT

45 1141 TTCACCACCC CCTGACCGCG AATGGTGAGA TTGAGAATAT AACCTTTCAT
TCCCAGCGGT
1201 CGGTCGATAA AAAAATCGAG ATAACCGTTG GCCTCAATCG GCGTTAAACC
CGCCACCAGA

50 1261 TGGGCATTAA ACGAGTATCC CGGCAGCAGG GGATCATTTT GCGCTTCAGC
CATACTTTTC Start araC

1321 ATACTCCCGC CATTTCAGAGA AGAAACCAAT TGTCCATATT GCATCAGACA
TTGCCGTCAC <--

55 1381 TCGTCTTTT ACTGGCTCTT CTCGCTAACC AAACCGGTAA CCCCCTTAT
TAAAAGCATT
1441 CTGTAACAAA GCGGGACCAA AGCCATGACA AAAACGCGTA ACAAAGTGT
CTATAATCAC

60 1501 GGCAGAAAAG TCCACATTGA TTATTTGCAC GGCGTCACAC TTTGCTATGC
CATAGCATTT
1561 TTATCCATAA GATTAGCGGA TCCTACCTGA CGCTTTTAT CGCAACTCTC
TACTGTTTCT

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1621 CCATACCCGT TTTTTTGGGC TAGCAGGAGG ^{SD} CCGTCGACTC ^{SalI} ~~TAGAGG~~GATCC
 CCGCGCCCTC

5

1681 ^{Stem-loop} ATCCGAAAGG ^{KpnI} GCGTATTGGT ACCGAGCTCG AATTCGTAAT CATGGTCATA
 GCTGTTTCCT

10

1741 GTGTGAAATT GTTATCCGCT CACAATTCCA CACAACATAC GAGCCGGAAG
 CATAAAGTGT
 1801 AAAGCCTGGG GTGCCTAATG AGTGAGCTAA CTCACATTAA TTGCGTTGCG
 CTCACTGCCC

15

1861 GCTTTCAGT CGGGAACCT GTCGTGCCAG CTGCATTAAT GAATCGGCCA
 ACGCGCGGGG
 1921 AGAGGCGGTT TCGTATTGG GCGCTCTTCC GCTTCCTCGC TCACTGACTC
 GCTGCGCTCG
 1981 GTCGTTGCGC TCGGCGGAGC GGTATCAGCT CACTCAAAGG CGGTAATACG
 GTTATCCACA

20

2041 GAATCAGGGG ATAACGCAGG AAAGAACATG TGAGCAAAAG GCCAGCAAAA
 GGCCAGGAAC
 2101 CGTAAAAAGG CCGCGTTGCT GCGCTTTTTT CATAGGCTCC GCCCCCTGA
 CGAGCATCAC

25

2161 AAAAATCGAC GCTCAAGTCA GAGGTGGCGA AACCCGACAG GACTATAAAG
 ATACCAGGCG
 2221 TTTCCCCCTG GAAGCTCCCT CGTGCGCTCT CCGTTCCGA CCCTGCCGCT
 TACCGGATAC
 2281 CTGTCCGCCT TTCTCCCTTC GGAAGCGTG GCGCTTTCTC ATAGCTCAGC
 CTGTAGGTAT

30

2341 CTCAGTTCGG TGTAGGTCGT TCGCTCCAAG CTGGGCTGTG TGCACGAACC
 CCCCCTTCAG
 2401 CCCGACCGCT GCGCCTTATC CGGTAACAT CTCTTGAGT CCAACCCGGT
 AAGACACGAC

35

2461 TTATCGCCAC TGGCAGCAGC CACTGGTAAC AGGATTAGCA GAGCGAGGTA
 TGTAGGCGGT
 2521 GCTACAGAGT TCTTGAAGTG GTGGCCTAAC TACGGCTACA CTAGAAGGAC
 AGTATTTGGT
 2581 ATCTGCGCTC TGCTGAAGCC AGTTACCTTC GGAAAAAGAG TTGGTAGCTC
 TTGATCCGGC

40

2641 AAACAAACCA CCGCTGGTAG CGGTGGTTTT TTTGTTTGCA AGCAGCAGAT
 TACGCGCAGA
 2701 AAAAAAGGAT CTCAAGAAGA TCCTTTGATC TTTTCTACGG GGTCTGACGC
 TCAGTGGAAC

45

2761 GAAACTCAC GTTAAGGGAT TTTGGTCATG AGATTATCAA AAAGGATCTT
 CACCTAGATC
 2821 CTTTTAAATT AAAAATGAAG TTTTAAATCA ATCTAAAGTA TATATGAGTA
 AACTTGGTCT
 2881 GACAGTTACC AATGCTTAAT CAGTGAGGCA CCTATCTCAG CGATCTGTCT
 ATTTTCGTTCA

50

2941 TCCATAGTTG CCTGACTCCC CGTCGTGTAG ATAACACGA TACGGGAGGG
 CTTACCATCT
 3001 GGCCCCAGTG CTGCAATGAT ACCGCGAGAC CCACGCTCAC CGGCTCCAGA
 TTTATCAGCA

55

3061 ATAAACCAGC CAGCCGGAAG GGCCGAGCGC AGAAGTGGTC CTGCAACTTT
 ATCCGCCTCC
 3121 ATCCAGTCTA TTAATTGTTG CCGGGAAGCT AGAGTAAGTA GTTCGCCAGT
 TAATAGTTTG
 3181 CGCAACGTTG TTGCCATTGC TACAGGCATC GTGGTGTAC GCTCGTCGTT
 TGGTATGGCT

60

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3241 TCATTCAGCT CCGGTTCCCA ACGATCAAGG CGAGTTACAT GATCCCCCAT
GTTGTGCAAA
3301 AAAGCGGTTA GCTCCTTCGG TCCTCCGATC GTTGTGAGAA GTAAGTTGGC
CGCAGTGTTA
5 3361 TCACTCATGG TTATGGCAGC ACTGCATAAT TCTCTTACTG TCATGCCATC
CGTAAGATGC
3421 TTTTCTGTGA CTGGTGAGTA CTCAACCAAG TCATTCTGAG AATAGTGTAT
GCGGCGACCG
3481 AGTTGCTCTT GCCCGGCGTC AATACGGGAT AATACCGCGC CACATAGCAG
10 AACTTTAAAA
3541 GTGCTCATCA TTGAAAACG TTCCTCGGGG CGAAACTCT CAAGGATCTT
ACCGCTGTTG
3601 AGATCCAGTT CGATGTAACC CACTCGTGCA CCCAACTGAT CTTCAGCATC
TTTTACTTTC
15 3661 ACCAGCGTTT CTGGGTGAGC AAAACAGGA AGGCAAAATG CCGCAAAAAA
GGGAATAAGG
3721 GCGACACGGA AATGTTGAAT ACTCATACTC TTCCTTTTTC AATATTATTG
AAGCATTAT
3781 CAGGGTTATT GTCTCATGAG CGGATACATA TTTGAATGTA TTTAGAAAAA
20 TAAACAAATA
3841 GGGGTTCGCG GCACATTTCC CCGAAAAGTG CCACCTGACG TCTAAGAAAC
CATTATTATC
3901 ATGACATTAA CCTATAAAAA TAGGCGTATC ACGAGGCCCT TTCGTC

25 The segment araC through Para was taken from pBAD24 using PCR added HindIII and modified aligned Shine-Delgarno (SD) sequence with Sall followed by XbaI, a stem-loop transcriptional stop sequence, and KpnI. The PCR product was cloned into pUC18 using HindIII and KpnI.

30 SEQ ID NO.: 152

pMPX-72 rhamnose-inducible expression vector

1 TCGCGCGTTT CCGTGATGAC GGTGAAAACC TCTGACACAT GCAGCTCCCG
35 GAGACGGTCA
61 CAGCTTGCTCT GTAAGCGGAT GCCGGGAGCA GACAAGCCCG TCAGGGCGCG
TCAGCGGGTG
121 TTGGCGGGTG TCGGGGCTGG CTTAACTATG CGGCATCAGA GCAGATTGTA
CTGAGAGTGC
40 181 ACCATATGCG GTGTGAAATA CCGCACAGAT GCGTAAGGAG AAAATACCGC
ATCAGGCGCC
241 ATTCGCCATT CAGGCTGCGC AACTGTTGGG AAGGGCGATC GGTGCGGGCC
TCTTCGCTAT
301 TACGCCAGCT GGCGAAAGGG GGATGTGCTG CAAGGCGATT AAGTTGGGTA
45 ACGCCAGGGT

Stop rhaR

361 TTTCCAGTC ACGACGTTGT AAAACGACGG CCAGTGCCAA GCTTAATTAA
TCTTTCTGCG
50

HindIII

421 AATTGAGATG ACGCCACTGG CTGGGCGTCA TCCCGGTTTC CCGGGTAAAC
ACCACCGAAA
481 AATAGTTACT ATCTTCAAAG CCACATTCGG TCGAAATATC ACTGATTAA
55 AGGCGGCTAT
541 GCTGGAGAAG ATATTGCGCA TGACACACTC TGACCTGTG CAGATATTGA
TTGATGGTCA

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601 TTCCAGTCTG CTGGCGAAAT TGCTGACGCA AAACGCGCTC ACTGCACGAT
GCCTCATCAC
661 AAAATTTATC CAGCGCAAAG GGACTTTTCA GGCTAGCCGC CAGCCGGGTA
ATCAGCTTAT
5 721 CCAGCAACGT TTCGCTGGAT GTTGGCGGCA ACGAATCACT GGTGTAACGA
TGGCGATTCA
781 GCAACATCAC CAACTGCCCC AACAGCAACT CAGCCATTTC GTTAGCAAAC
GGCACATGCT
841 GACTACTTTC ATGCTCAAGC TGACCGATAA CCTGCCGCGC CTGCGCCATC
10 CCCATGCTAC
901 CTAAGCGCCA GTGTGGTTGC CCTGCGCTGG CGTTAAATCC CGGAATCGCC
CCCTGCCAGT
961 CAAGATTTCAG CTTCAGACGC TCCGGGCAAT AAATAATATT CTGCAAAACC
AGATCGTTAA
15 1021 CGGAAGCGTA GGAGTGTTTA TCGTCAGCAT GAATGTAAAA GAGATCGCCA
CGGGTAATGC
1081 GATAAGGGCG ATCGTTGAGT ACATGCAGGC CATTACCGCG CCAGACAATC
ACCAGCTCAC
1141 AAAAATCATG TGTATGTTCA GCAAAGACAT CTTGCCGATA ACGGTCAGCC
20 ACAGCGACTG
1201 CCTGCTGGTC GCTGGCAAAA AAATCATCTT TGAGAAGTTT TAACTGATGC
GCCACCGTGG
1261 CTACCTCGGC CAGAGAACGA AGTTGATTAT TCGCAATATG GCGTACAAAT
ACGTTGAGAA
25
Stop rhaS Start rhaR
1321 GATTTCGCGT TT ATTGCAGAAA GCCAT CCCCCT CCCTGGCGAA TATCACGCGG
TGACCAGTTA
<--
30
1381 AACTCTCGGC GAAAAAGCGT CGAAAAGTGG TTACTGTCGC TGAATCCACA
GCGATAGGCG
1441 ATGTCAGTAA CGCTGGCCTC GCTGTGGCGT AGCAGATGTC GGGCTTTCAT
CAGTCGCAGG
35 1501 CGGTTTCAGGT ATCGCTGAGG CGTCAGTCCC GTTTGCTGCT TAAGCTGCCG
ATGTAGCGTA
1561 CGCAGTGAAA GAGAAAATTG ATCCGCCACG GCATCCCAAT TCACCTCATC
GGCAAAATGG
1621 TCCTCCAGCC AGGCCAGAAG CAAGTTGAGA CGTGATGCGC TGTTTTCCAG
40 GTTCTCCTGC
1681 AAAC TGCTTT TACGCAGCAA GAGCAGTAAT TGCATAAACA AGATCTCGCG
ACTGGCGGTC
1741 GAGGGTAAAT CATTTTCCCC TTCCTGCTGT TCCATCTGTG CAACCAGCTG
TCGCACCTGC
45 1801 TGCAATACGC TGTGGTTAAC GCGCCAGTGA GACGGATACT GCCCATCCAG
CTCTTGTTGGC
1861 AGCAACTGAT TCAGCCCAGC GAGAACTGA AATCGATCCG GCGAGCGATA
CAGCACATTG
1921 GTCAGACACA GATTATCGGT ATGTTTCATAC AGATGCCGAT CATGATCGCG
50 TACGAAACAG
1981 ACCGTGCCAC CGGTGATGGT ATAGGGCTGC CCATTAAACA CATGAATACC
CGTGCCATGT
2041 TCGACAATCA CAATTTTCATG AAAATCATGA TGATGTTTCAG GAAAATCCGC
CTGCGGGAGC
55 2101 CGGGGTTCTA TCGCCACGGA CGCGTTACCA GACGGAAAAA AATCCACACT
ATGTAATACG
Start rhaS
2161 GTCATACTGG CCTCCTGATG TCGTCAACAC GGCGAAATAG TAATCACGAG
60 GTCAGGTTCT

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<--

2221 TACCTTAAAT TTTCGACGGA AAACCACGTA AAAAACGTCG ATTTTTC AAG
ATACAGCGTG
5 2281 AATTTTCAGG AAATGCGGTG AGCATCACAT CACCACAATT CAGCAAATTG
TGAACATCAT
2341 CACGTTTCATC TTCCCTGGT TGCCAATGGC CCATTTTCCT GTCAGTAACG
AGAAGGTCGC

10 2401 GAATTCAGGC GCTTTTTAGA CTGGTCGTAA TGAAATTCAG GAGGTTCTGC
AGGTCGACTC SD PstI SalI

15 2461 TAGAGGATCC CCGCGCCCTC ATCCGAAAGG GCGTATTGGT ACCGAGCTCG
AATTCGTAAT XbaI Stem-loop KpnI

2521 CATGGTCATA GCTGTTTCCT GTGTGAAATT GTTATCCGCT CACAATTCCA
CACACATAC
20 2581 GAGCCGGAAG CATAAAGTGT AAAGCCTGGG GTGCCTAATG AGTGAGCTAA
CTCACATTAA
2641 TTGCGTTGCG CTCACTGCCC GCTTTCAGT CGGGAAACCT GTCGTGCCAG
CTGCATTAAT
2701 GAATCGGCCA ACGCGCGGGG AGAGGCGGTT TGCCTATTGG GCGCTCTTCC
25 GCTTCCTCGC
2761 TCACTGACTC GCTGCGCTCG GTCGTTCCGGC TCGGCGGAGC GGTATCAGCT
CACTCAAAGG
2821 CGGTAATACG GTTATCCACA GAATCAGGGG ATAACGCAGG AAAGAACATG
TGAGCAAAAG
30 2881 GCCAGCAAAA GGCCAGGAAC CGTAAAAAGG CCGCGTTGCT GGCGTTTTTC
CATAGGCTCC
2941 GCCCCCTGA CGAGCATCAC AAAAATCGAC GCTCAAGTCA GAGGTGGCGA
AACCCGACAG
3001 GACTATAAAG ATACCAGGCG TTTCCCCCTG GAAGCTCCCT CGTGCGCTCT
35 CCTGTTCCGA
3061 CCCTGCCGCT TACCGGATAC CTGTCCGCCT TTCTCCCTTC GGAAGCGTG
GCGCTTTCTC
3121 ATAGCTCAGC CTGTAGGTAT CTCAGTTCGG TGTAGGTCGT TCGCTCCAAG
CTGGGCTGTG
40 3181 TGCACGAACC CCCCCTTCAG CCGACCGCT GCGCCTTATC CGGTAACTAT
CGTCTTGAGT
3241 CCAACCCGGT AAGACACGAC TTATCGCCAC TGGCAGCAGC CACTGGTAAC
AGGATTAGCA
3301 GAGCGAGGTA TGTAGGCGGT GCTACAGAGT TCTTGAAGTG GTGGCCTAAC
45 TACGGCTACA
3361 CTAGAAGGAC AGTATTTGGT ATCTGCGCTC TGCTGAAGCC AGTTACCTTC
GGAAAAAGAG
3421 TTGGTAGCTC TTGATCCGGC AAACAAACCA CCGCTGGTAG CGGTGGTTTT
TTTGTTTGCA
50 3481 AGCAGCAGAT TACGCGCAGA AAAAAAGGAT CTCAAGAAGA TCCTTTGATC
TTTTCTACGG
3541 GGTCTGACGC TCAGTGGAAC GAAAACTCAC GTTAAGGGAT TTTGGTCATG
AGATTATCAA
3601 AAAGGATCTT CACCTAGATC CTTTTAAATT AAAAATGAAG TTTTAAATCA
55 ATCTAAAGTA
3661 TATATGAGTA AACTTGGTCT GACAGTTACC AATGCTTAAT CAGTGAGGCA
CCTATCTCAG
3721 CGATCTGTCT ATTTGTTCA TCCATAGTTG CCTGACTCCC CGTCGTGTAG
ATAACTACGA

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3781 TACGGGAGGG CTTACCATCT GGCCCCAGTG CTGCAATGAT ACCGCGAGAC
CCACGCTCAC
3841 CGGCTCCAGA TTTATCAGCA ATAAACCAGC CAGCCGGAAG GGCCGAGCGC
AGAAGTGGTC
5 3901 CTGCAACTTT ATCCGCCTCC ATCCAGTCTA TTAATTGTTG CCGGGAAGCT
AGAGTAAGTA
3961 GTTCGCCAGT TAATAGTTTG CGCAACGTTG TTGCCATTGC TACAGGCATC
GTGGTGTAC
4021 GCTCGTCGTT TGGTATGGCT TCATTAGCT CCGGTTCCCA ACGATCAAGG
10 CGAGTTACAT
4081 GATCCCCCAT GTTGTGCAAA AAAGCGGTTA GCTCCTTCGG TCCTCCGATC
GTTGTGAGAA
4141 GTAAGTTGGC CGCAGTGTTA TCACTCATGG TTATGGCAGC ACTGCATAAT
TCTCTTACTG
15 4201 TCATGCCATC CGTAAGATGC TTTTCTGTGA CTGGTGAGTA CTCAACCAAG
TCATTCTGAG
4261 AATAGTGTAT GCGGCGACCG AGTTGCTCTT GCCCGGCGTC AATACGGGAT
AATACGCGC
4321 CACATAGCAG AACTTTAAAA GTGCTCATCA TTGGAAAACG TTCTTCGGGG
20 CGAAAACCTCT
4381 CAAGGATCTT ACCGCTGTTG AGATCCAGTT CGATGTAACC CACTCGTGCA
CCCAACTGAT
4441 CTTCAGCATC TTTTACTTTC ACCAGCGTTT CTGGGTGAGC AAAAACAGGA
AGGCCAAAATG
25 4501 CCGCAAAAAA GGGAATAAGG GCGACACGGA AATGTTGAAT ACTCATACTC
TTCCTTTTTT
4561 AATATTATTG AAGCATTTAT CAGGGTTATT GTCTCATGAG CGGATACATA
TTTGAATGTA
4621 TTTAGAAAAA TAAACAAATA GGGGTTCCGC GCACATTTC CCGAAAAGTG
30 CCACCTGACG
4681 TCTAAGAAAC CATTATTATC ATGACATTAA CCTATAAAAA TAGGCGTATC
ACGAGGCCCT
4741 TTCGTC

35 The segment rhaR through PriA was taken from the E. coli chromosome using PCR added
HindIII and modified aligned Shine-Delgarno (SD) sequence with PstI followed by SalI, XbaI, a
stem-loop transcriptional stop sequence, and KpnI. The PCR product was cloned into pUC18
using HindIII and KpnI.

40

SEQ ID NO.: 153

pMPX-67 rhamnose-inducible expression vector

45

1 TCGCGCGTTT CGGTGATGAC GGTGAAAACC TCTGACACAT GCAGCTCCCG
GAGACGGTCA
61 CAGCTTGTCT GTAAGCGGAT GCCGGGAGCA GACAAGCCCG TCAGGGCGCG
TCAGCGGGTG
50 121 TTGGCGGGTG TCGGGGCTGG CTTAACTATG CGGCATCAGA GCAGATTGTA
CTGAGAGTGC
181 ACCATATGCG GTGTGAAATA CCGCACAGAT GCGTAAGGAG AAAATACCGC
ATCAGGCGCC
241 ATTCGCCATT CAGGCTGCGC AACTGTTGGG AAGGGCGATC GGTGCGGGCC
55 TCTTCGCTAT
301 TACGCCAGCT GGCGAAAGGG GGATGTGCTG CAAGGCGATT AAGTTGGGTA
ACGCCAGGGT

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3361 GGACAGTATT TGGTATCTGC GCTCTGCTGA AGCCAGTTAC CTTCGGAAAA
AGAGTTGGTA
3421 GCTCTTGATC CGGCAAACAA ACCACCGCTG GTAGCGGTGG TTTTTTTGTT
TGCAAGCAGC
5 3481 AGATTACGCG CAGAAAAAAA GGATCTCAAG AAGATCCTTT GATCTTTTCT
ACGGGGTCTG
3541 ACGCTCAGTG GAACGAAAAC TCACGTTAAG GGATTTTGGT CATGAGATTA
TCAAAAAGGA
3601 TCTTCACCTA GATCCTTTTA AATTAAAAAT GAAGTTTAA ATCAATCTAA
10 AGTATATATG
3661 AGTAAACTTG GTCTGACAGT TACCAATGCT TAATCAGTGA GGCACCTATC
TCAGCGATCT
3721 GTCTATTTTCG TTCATCCATA GTTGCCTGAC TCCCCGTCGT GTAGATAACT
ACGATACGGG
15 3781 AGGGCTTACC ATCTGGCCCC AGTGCTGCAA TGATACCGCG AGACCCACGC
TCACCGGCTC
3841 CAGATTTATC AGCAATAAAC CAGCCAGCCG GAAGGGCCGA GCGCAGAAGT
GGTCCTGCAA
3901 CTTTATCCGC CTCCATCCAG TCTATTAATT GTTGCCGGGA AGCTAGAGTA
20 AGTAGTTCGC
3961 CAGTTAATAG TTTGCGCAAC GTTGTGCGCA TTGCTACAGG CATCGTGGTG
TCACGCTCGT
4021 CGTTTGGTAT GGCTTCATTC AGCTCCGGTT CCCAACGATC AAGGCGAGTT
ACATGATCCC
25 4081 CCATGTTGTG CAAAAAGCG GTTAGCTCCT TCGGTCCTCC GATCGTTGTC
AGAAGTAAGT
4141 TGGCCGCACT GTTATCACTC ATGGTTATGG CAGCACTGCA TAATTCTCTT
ACTGTCATGC
4201 CATCCGTAAG ATGCTTTTCT GTGACTGGTG AGTACTCAAC CAAGTCATTC
30 TGAGAATAGT
4261 GTATGCGGCG ACCGAGTTGC TCTTGCCCGG CGTCAATACG GGATAATACC
GCGCCACATA
4321 GCAGAACTTT AAAAGTGCTC ATCATTGGAA AACGTTCTTC GGGGCGAAAA
CTCTCAAGGA
35 4381 TCTTACCGCT GTTGAGATCC AGTTCGATGT AACCCACTCG TGCACCCAAC
TGATCTTCAG
4441 CATCTTTTAC TTTCACCAGC GTTTCTGGGT GAGCAAAAAC AGGAAGGCAA
AATGCCGCAA
4501 AAAAGGGAAT AAGGGCGACA CGGAAATGTT GAATACTCAT ACTCTTCCTT
40 TTCAATATT
4561 ATTGAAGCAT TTATCAGGGT TATTGTCTCA TGAGCGGATA CATATTTGAA
TGTATTTAGA
4621 AAAATAAACA AATAGGGGTT CCGCGCACAT TTCCCCGAAA AGTGCCACCT
GACGTCTAAG
45 4681 AAACCATTAT TATCATGACA TTAACCTATA AAAATAGGCG TATCAGGAG
CCCTTTCGTC

The segment rhaR through Prha was taken from the E. coli chromosome using PCR added
HindIII and modified aligned Shine-Delgarno (SD) sequence with SalI followed by XbaI, a stem-
50 loop transcriptional stop sequence, and KpnI. The PCR product was cloned into pUC18 using
HindIII and KpnI.

SEQ ID NO.: 154

55

pMPX-71 arabinose-inducible expression vector

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1 TCGCGCGTTT CGGTGATGAC GGTGAAAACC TCTGACACAT GCAGCTCCCC
GAGACGGTCA
61 CAGCTTGTCT GTAAGCGGAT GCCGGGAGCA GACAAGCCCC TCAGGGCGCG
TCAGCGGGTG
5 121 TTGGCGGGTG TCGGGGCTGG CTTAACTATG CGGCATCAGA GCAGATTGTA
CTGAGAGTGC
181 ACCATATGCG GTGTGAAATA CCGCACAGAT GCGTAAGGAG AAAATACCGC
ATCAGGCGCC
241 ATTCGCCATT CAGGCTGCGC AACTGTTGGG AAGGGCGATC GGTGCGGGCC
10 TCTTCGCTAT
301 TACGCCAGCT GGCGAAAGGG GGATGTGCTG CAAGGCGATT AAGTTGGGTA
ACGCCAGGGT

HindIII

15 361 TTTCCAGTC ACGACGTTGT AAAACGACGG CCAGTGCCAA GCTTCAAGC
GTCAATTGTC

Stop araC

20 421 TGATTCGTTA CCAATTTATGA CAACTTGACG GCTACATCAT TCACTTTTTT
TTCACAACCG
481 GCACGGAAC TCGCTCGGGCT GGCCCCGGTG CATTTTTTAA ATACCCGCGA
GAAATAGAGT
541 TGATCGTCAA AACCAACATT GCGACCGACG GTGGCGATAG GCATCCGGGT
GGTGCTCAAA
25 601 AGCAGCTTCG CCTGGCTGAT ACGTTGGTCC TCGCGCCAGC TTAAGACGCT
AATCCCTAAC
661 TGCTGGCGGA AAAGATGTGA CAGACGCGAC GGCGACAAGC AAACATGCTG
TGCGACGCTG
721 GCGATATCAA AATTGCTGTC TGCCAGGTGA TCGCTGATGT ACTGACAAGC
30 CTCGCGTACC
781 CGATTATCCA TCGGTGGATG GAGCGACTCG TTAATCGCTT CCATGCGCCG
CAGTAACAAT
841 TGCTCAAGCA GATTTATCGC CAGCAGCTCC GAATAGCGCC CTTCCCCTTG
CCCGGCGTTA
35 901 ATGATTTGCC CAAACAGGTC GCTGAAATGC GGCTGGTGCG CTTTCATCCG
GCGAAAGAAC
961 CCCGTATTGG CAAATATTGA CGGCCAGTTA AGCCATTCAT GCCAGTAGGC
GCGCGGACGA
1021 AAGTAAACCC ACTGGTGATA CCATTGCGGA GCCTCCGGAT GACGACCGTA
40 GTGATGAATC
1081 TCTCCTGGCG GGAACAGCAA AATATCACCC GGTGCGCAAA CAAATTCTCG
TCCCTGATTT
1141 TTCACCACCC CCTGACCGCG AATGGTGAGA TTGAGAATAT AACCTTTCAT
TCCCAGCGGT
45 1201 CGGTCGATAA AAAAATCGAG ATAACCGTTG GCCTCAATCG GCGTTAAAC
CGCCACCAGA
1261 TGGGCATTAA ACGAGTATCC CGGCAGCAGG GGATCATTTT GCGCTTCAGC
CATACTTTTC

Start araC

50 1321 ATACTCCCGC CATTCAGAGA AGAAACCAAT TGTCCATATT GCATCAGACA
TTGCCGTCAC

<--

55 1381 TGCGTCTTTT ACTGGCTCTT CTCGCTAACC AAACCGGTAA CCCCCTTAT
TAAAAGCATT
1441 CTGTAACAAA GCGGGACCAA AGCCATGACA AAAACGCGTA ACAAAGTGT
CTATAATCAC
1501 GGCAGAAAAG TCCACATTGA TTATTTGCAC GCGTCACAC TTTGCTATGC
60 CATAGCATTT

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1561 TTATCCATAA GATTAGCGGA TCCTACCTGA CGCTTTTATAT CGCAACTCTC
TACTGTTTCT

5 1621 CCATACCCGT TTTTTTGGGC TAGCAGGAGG ^{SD} ^{PstI} ^{SalI} ^{XbaI} CCCTGCAGGT CGACTCTAGA
GGATCCCCGC

10 1681 ^{Stem-loop} GCCCTCATCC GAAAGGGCGT ^{KpnI} ATTGGTACCG AGCTCGAATT CGTAATCATG
GTCATAGCTG

15 1741 TTTCTGTGT GAAATTGTTA TCCGCTCACA ATTCCACACA ACATACGAGC
CGGAAGCATA
1801 AAGTGTAAG CCTGGGGTGC CTAATGAGTG AGCTAACTCA CATTAAATTGC
GTTGCGCTCA
1861 CTGCCCCTT TCCAGTCGGG AAACCTGTCTG TGCCAGCTGC ATTAATGAAT
CGGCCAACGC
1921 GCGGGGAGAG GCGGTTTGCG TATTGGGCGC TCTTCCGCTT CCTCGCTCAC
TGACTCGCTG

20 1981 CGCTCGGTCTG TTCGGCTGCG GCGAGCGGTA TCAGCTCACT CAAAGGCGGT
AATACGGTTA
2041 TCCACAGAAAT CAGGGGATAA CGCAGGAAAG AACATGTGAG CAAAAGGCCA
GCAAAAGGCC
2101 AGGAACCGTA AAAAGGCCGC GTTGCTGGCG TTTTCCATA GGCTCCGCCC
CCCTGACGAG

25 2161 CATCACAAA ATCGACGCTC AAGTCAGAGG TGGCGAAACC CGACAGGACT
ATAAAGATAC
2221 CAGGCGTTTC CCCCTGGAAG CTCCTCTGTC CGCTCTCCTG TTCCGACCTT
GCCGCTTACC

30 2281 GGATACCTGT CCGCCTTTCT CCCTTCGGGA AGCGTGGCGC TTTCTCATAG
CTCACGCTGT
2341 AGGTATCTCA GTTCGGTGTA GGTCTGTCGC TCCAAGCTGG GCTGTGTGCA
CGAACCCCCC
2401 GTTCAGCCCG ACCGCTGCGC CTTATCCGGT AACTATCGTC TTGAGTCCAA
CCCGTAAGA

35 2461 CACGACTTAT CGCCACTGGC AGCAGCCACT GGTAACAGGA TTAGCAGAGC
GAGGTATGTA
2521 GCGGTGCTA CAGAGTTCTT GAAGTGGTGG CCTAACTACG GCTACACTAG
AAGGACAGTA

40 2581 TTTGGTATCT GCGCTCTGCT GAAGCCAGTT ACCTTCGGAA AAAGAGTTGG
TAGCTCTTGA
2641 TCCGGCAAAC AAACCACCGC TGGTAGCGGT GGTTTTTTTG TTTGCAAGCA
GCAGATTACG

45 2701 CGCAGAAAAA AAGGATCTCA AGAAGATCCT TTGATCTTTT CTACGGGGTC
TGACGCTCAG
2761 TGGAACGAAA ACTCACGTTA AGGGATTTTG GTCATGAGAT TATCAAAAAG
GATCTTCACC
2821 TAGATCCTTT TAAATTAAAA ATGAAGTTTT AAATCAATCT AAAGTATATA
TGAGTAAACT

50 2881 TGGTCTGACA GTTACCAATG CTTAATCAGT GAGGCACCTA TCTCAGCGAT
CTGTCTATTT
2941 CGTTCATCCA TAGTTGCCTG ACTCCCCGTC GTGTAGATAA CTACGATACG
GGAGGGCTTA

55 3001 CCATCTGGCC CCAAGTCTGC AATGATACCG CGAGACCCAC GCTCACCGGC
TCCAGATTTA
3061 TCAGCAATAA ACCAGCCAGC CGGAAGGGCC GAGCGCAGAA GTGGTCCTGC
AACTTTATCC
3121 GCCTCCATCC AGTCTATTAA TTGTTGCCGG GAAGCTAGAG TAAGTAGTTC
GCCAGTTAAT

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3181 AGTTTGCGCA ACGTTGTTGC CATTGCTACA GGCATCGTGG TGTCACGCTC
GTCGTTTGGT
3241 ATGGCTTCAT TCAGCTCCGG TTCCCAACGA TCAAGGCGAG TTACATGATC
CCCCATGTTG
5 3301 TGCAAAAAAG CGGTTAGCTC CTTCCGGTCCT CCGATCGTTG TCAGAAGTAA
GTTGGCCGCA
3361 GTGTTATCAC TCATGGTTAT GGCAGCACTG CATAATTCTC TTA CTGTGTCAT
GCCATCCGTA
3421 AGATGCTTTT CTGTGACTGG TGAGTACTCA ACCAAGTCAT TCTGAGAATA
10 GTGTATGCGG
3481 CGACCGAGTT GCTCTTGCCC GGC GTCAATA CGGGATAATA CCGCGCCACA
TAGCAGAACT
3541 TTAAAAAGTGC TCATCATTGG AAAACGTTCT TCGGGGCGAA AACTCTCAAG
GATCTTACCG
15 3601 CTGTTGAGAT CCAGTTCGAT GTAACCCACT CGTGACCCCA ACTGATCTTC
AGCATCTTTT
3661 ACTTTCACCA GCGTTTCTGG GTGAGCAAAA ACAGGAAGGC AAAATGCCGC
AAAAAAGGGA
3721 ATAAGGGCGA CACGGAAATG TTGAATACTC ATACTCTTCC TTTTTC AATA
20 TTATTGAAGC
3781 ATTTATCAGG GTTATTGTCT CATGAGCGGA TACATATTTG AATGTATTTA
GAAAAATAAA
3841 CAAATAGGGG TTCCGCGCAC ATTTCCCCGA AAAGTGCCAC CTGACGTCTA
AGAAACCATT
25 3901 ATTATCATGA CATTACCTA TAAAAATAGG CGTATCACGA GGCCCTTTCG TC

The segment araC through Para was taken from pBAD24 using PCR added HindIII and modified
aligned Shine-Delgarno (SD) sequence with PstI followed by Sall, XbaI, a stem-loop
transcriptional stop sequence, and KpnI. The PCR product was cloned into pUC18 using HindIII
30 and KpnI.

SEQ ID NO.: 155

35 pMPX-68 melibiose-inducible expression vector

1 TCGCGCGTTT CCGTGATGAC GGTGAAAACC TCTGACACAT GCAGCTCCCCG
GAGACGGTCA
61 CAGCTTGTCT GTAAGCGGAT GCCGGGAGCA GACAAGCCCCG TCAGGGCGCG
40 TCAGCGGGTG
121 TTGGCGGGTG TCGGGGCTGG CTTAACTATG CGGCATCAGA GCAGATTGTA
CTGAGAGTGC
181 ACCATATGCG GTGTGAAATA CCGCACAGAT GCGTAAGGAG AAAATACCGC
ATCAGGCGCC
45 241 ATTCGCCATT CAGGCTGCGC AACTGTTGGG AAGGGCGATC GGTGCGGGCC
TCTTCGCTAT
301 TACGCCAGCT GGC GAAAGGG GGATGTGCTG CAAGGCGATT AAGTTGGGTA
ACGCCAGGGT

50 361 TTTCCAGTC ACGACGTTGT AAAACGACGG CCAGTGCCAA GCTTTTAGCC
GGGAAACGTC

HindIII
Stop MelR

55 421 TGGCGGCGCT GTTGGCTAAG TTTGCGGTAT TGTTGCGGCG ACATGCCGAC
ATATTTGCCG
481 AACGTGCTGT AAAACGACT ACTTGAACGA AAGCCTGCCG TCAGGGCAAT
ATCGAGAATA

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541 CTTTATATCGG TATCGCTCAG TAACGCGCGA ACGTGGTTGA TGCGCATCGC
 GGTAATGTAC
 601 TGTTCATCG TCAATTGCAT GACCCGCTGG AATATCCCCA TTGCATAGTT
 GCGGTTAAGT
 5 661 TTGACGTGCT CAGCCACATC GTTGATGGTC AGCGCCTGAT CATAGTTTTC
 GGCAATAAAG
 721 CCCAGCATCT GGCTAACATA AAATTGCGCA TGGCGCGAGA CGCTGTTTTT
 GTGTGTGCGC
 781 GAGGTTTTAT TGACCAGAAT CGGTTCCCAG CCAGAGAGGC TAAATCGCTT
 10 GAGCATCAGG
 841 CCAATTTTCAT CAATGGCGAG CTGGCGAATT TGCTCGTTTCG GACTGTTTAA
 TTCCTGCTGC
 901 CAGCGGCGCA CTCAAACGG GCTAAGTTGC TGTGTGGCCA GTGATTTGAT
 CACCATGCCG
 15 961 TGAGTGACGT GGTAAATCAG GTCTTTATCC AGCGGCCAGG AGAGAAACAG
 ATGCATCGGC
 1021 AGATTAAAAA TCGCCATGCT CTGACAGGTT CCGGTATCTG TTAGTTGGTG
 CGGTGTACAG
 1081 GCCCAGAAC ACGTGATATG ACCCTGATTG ATATTCACCT TTTCATTGTT
 20 GATCAGGTAT
 1141 TCCACATCGC CATCGAAAG CACATTCCT TCGACCTGAC CATGCCAGTG
 GCTGGTGGGC
 1201 ATGATATGCG GTGCGCGAAA CTCAATCTCC ATCCGCTGGT ATTCCGAATA
 CAGCGACAGC
 25
 1261 GGGCTGCGGG TCTGTTTTTC GTCGCTGCTG CACATAAACG TATCTGTATT
CATGGATGGC +1 MelR
 30
 1321 TCTCTTTCCT GGAATATCAG AATTATGGCA GGAGTGAGGG AGGATGACTG
 CGAGTGGGAG
 1381 CACGGTTTTTC ACCCTCTTCC CAGAGGGGCG AGGGGACTCT CCGAGTATCA
 TGAGGCCGAA
 35 1441 AACTCTGCTT TTCAGGTAAT TTATTCCCAT AAATCAGAT TTAGTGCTGC
 TTCACGCAAG
 1501 ATCTGAGTTT ATGGGAATGC TCAACCTGGA AGCCGGAGGT TTTCTGCAGA
 TTCGCCTGCC
 40
 1561 ATGATGAAGT TATTCAAGCA AGCCAGGAGG TCGTCGACTC TAGAGGATCC
 CCGCGCCCTC SD SalI XbaI
 45
 1621 ATCCGAAAGG GCGTATTGGT ACCGAGCTCG AATTCGTAAT CATGGTCATA
 GCTGTTTCCT Stem-loop KpnI
 50
 1681 GTGTGAAATT GTTATCCGCT CACAATTCCA CACAACATAC GAGCCGGAAG
 CATAAAGTGT
 1741 AAAGCCTGGG GTGCCTAATG AGTGAGCTAA CTCACATTAA TTGCGTTGCG
 CTCACTGCCC
 1801 GCTTTCAGT CGGGAAACCT GTCGTGCCAG CTGCATTAAAT GAATCGGCCA
 ACGCGCGGGG
 55 1861 AGAGGCGGTT TGCGTATTGG GCGCTCTTCC GCTTCCTCGC TCACTGACTC
 GCTGCGCTCG
 1921 GTCGTTGCGC TGCGGCGAGC GGTATCAGCT CACTCAAAGG CGGTAATACG
 GTTATCCACA
 1981 GAATCAGGGG ATAACGCAGG AAAGAACATG TGAGCAAAAG GCCAGCAAAA
 60 GGCCAGGAAC

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2041 CGTAAAAAGG CCGCGTTGCT GGCCTTTTTT CATAGGCTCC GCCCCCTGA
CGAGCATCAC
2101 AAAAATCGAC GCTCAAGTCA GAGGTGGCGA AACCCGACAG GACTATAAAG
ATACCAGGCG
5 2161 TTTCCCCCTG GAAGCTCCCT CGTGCGCTCT CCTGTTCCGA CCCTGCCGCT
TACCGGATAC
2221 CTGTCCGCCT TTCTCCCTTC GGGAAAGCGTG GCGCTTTCTC ATAGCTCACG
CTGTAGGTAT
2281 CTCAGTTCGG TGTAGGTCGT TCGCTCCAAG CTGGGCTGTG TGCACGAACC
10 CCCCGTTCAG
2341 CCCGACCGCT GCGCCTTATC CGGTAACTAT CGTCTTGAGT CCAACCCGGT
AAGACACGAC
2401 TTATCGCCAC TGGCAGCAGC CACTGGTAAC AGGATTAGCA GAGCGAGGTA
TGTAGGCGGT
15 2461 GCTACAGAGT TCTTGAAGTG GTGGCCTAAC TACGGCTACA CTAGAAGGAC
AGTATTTGGT
2521 ATCTGCGCTC TGCTGAAGCC AGTTACCTTC GGAAAAAGAG TTGGTAGCTC
TTGATCCGGC
2581 AAACAAACCA CCGCTGGTAG CGGTGGTTTT TTTGTTTGCA AGCAGCAGAT
20 TACGCGCAGA
2641 AAAAAAGGAT CTCAAGAAGA TCCTTTGATC TTTTCTACGG GGTCTGACGC
TCAGTGGAAC
2701 GAAAACCTAC GTTAAGGGAT TTTGGTCATG AGATTATCAA AAAGGATCTT
CACCTAGATC
25 2761 CTTTTAAAT TAAAAATGAAG TTTTAAATCA ATCTAAAGTA TATATGAGTA
AACTTGGTCT
2821 GACAGTTACC AATGCTTAAT CAGTGAGGCA CCTATCTCAG CGATCTGTCT
ATTTCTGTTCA
2881 TCCATAGTTG CCTGACTCCC CGTCGTGTAG ATAACCTACGA TACGGGAGGG
30 CTTACCATCT
2941 GGCCCCAGTG CTGCAATGAT ACCGCGAGAC CCACGCTCAC CGGCTCCAGA
TTTATCAGCA
3001 ATAAACCAGC CAGCCGGAAG GGCCGAGCGC AGAAGTGGTC CTGCAACTTT
ATCCGCCTCC
35 3061 ATCCAGTCTA TTAATTGTTG CCGGAAGCT AGAGTAAGTA GTTCGCCAGT
TAATAGTTTG
3121 CGCAACGTTG TTGCCATTGC TACAGGCATC GTGGTGTAC GCTCGTCGTT
TGGTATGGCT
3181 TCATTAGCT CCGGTTCCCA ACGATCAAGG CGAGTTACAT GATCCCCCAT
40 GTTGTGCAAA
3241 AAAGCGGTTA GCTCCTTCGG TCCTCCGATC GTTGTGAGAA GTAAGTTGGC
CGCAGTGTTA
3301 TCATCATGG TTATGGCAGC ACTGCATAAT TCTCTTACTG TCATGCCATC
CGTAAGATGC
45 3361 TTTTCTGTGA CTGGTGAGTA CTCAACCAAG TCATTCTGAG AATAGTGTAT
GCGGCGACCG
3421 AGTTGCTCTT GCGGCGGCTC AATACGGGAT AATACCGCGC CACATAGCAG
AACTTTAAAA
3481 GTGCTCATCA TTGAAAACG TTCTTCGGGG CGAAAACTCT CAAGGATCTT
50 ACCGCTGTTG
3541 AGATCCAGTT CGATGTAACC CACTCGTGCA CCCAACTGAT CTTCAGCATC
TTTTACTTTC
3601 ACCAGCGTTT CTGGGTGAGC AAAAAAGGA AGGCAAAATG CCGCAAAAAA
GGGAATAAGG
55 3661 GCGACACGGA AATGTTGAAT ACTCATACTC TTCCTTTTTT AATATTATTG
AAGCATTTAT
3721 CAGGGTTATT GTCTCATGAG CGGATACATA TTTGAATGTA TTTAGAAAAA
TAAACAAATA
3781 GGGGTTCCGC GCACATTTCC CCGAAAAGTG CCACCTGACG TCTAAGAAAC
60 CATTATTATC

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3841 ATGACATTAA CCTATAAAAA TAGGCGTATC ACGAGGCCCT TTCGTC

SEQ ID NO.: 166

5

MalE (1-370) Factor Xa NTR (43-424) FLAG

SalI +1 MalE (1-370)

1 GTCGACATGAAAATAAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAAACGACGATGATGTTT

10 1 M K I K T G A R I L A L S A L T T M M F

61 TCCGCCTCGGCTCTCGCCAAAATCGAAGAAGGTAAACTGGTAATCTGGATTAAACGGCGAT

21 S A S A L A K I E E G K L V I W I N G D

15 121 AAAGGCTATAACGGTCTCGCTGAAGTCGGTAAGAAATTTCGAGAAAGATACCGGAATTAAA

41 K G Y N G L A E V G K K F E K D T G I K

181 GTCACCGTTGAGCATCCGGATAAACTGGAAGAGAAAATTCCCACAGGTTGCGGCAACTGGC

61 V T V E H P D K L E E K F P Q V A A T G

20 241 GATGGCCCTGACATTATCTTCTGGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGC

81 D G P D I I F W A H D R F G G Y A Q S G

301 CTGTTGGCTGAAATCACCCCGACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGG

25 101 L L A E I T P D K A F Q D K L Y P F T W

361 GATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCG

121 D A V R Y N G K L I A Y P I A V E A L S

30 421 CTGATTTATAACAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCG

141 L I Y N K D L L P N P P K T W E E I P A

481 CTGGATAAAGAAGCTGAAAGCGAAAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCG

161 L D K E L K A K G K S A L M F N L Q E P

35 541 TACTTCACCTGGCCGCTGATTGCTGCTGACGGGGGTTATGCGTTCAAGTATGAAAACGGC

181 Y F T W P L I A A D G G Y A F K Y E N G

601 AAGTACGACATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTC

40 201 K Y D I K D V G V D N A G A K A G L T F

661 CTGGTTGACCTGATTAATAAACAAACACATGAATGCAGACACCGATTACTCCATCGCAGAA

221 L V D L I K N K H M N A D T D Y S I A E

45 721 GCTGCCTTTAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAAC

241 A A F N K G E T A M T I N G P W A W S N

781 ATCGACACCAGCAAAGTGAATTATGGTGTAACGGTACTGCCGACCTTCAAGGGTCAACCA

261 I D T S K V N Y G V T V L P T F K G Q P

50 841 TCCAAACCGTTGTTGGCGTGCTGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAG

281 S K P F V G V L S A G I N A A S P N K E

901 CTGGCGAAAGAGTTCTCGAAAACCTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAAT

55 301 L A K E F L E N Y L L T D E G L E A V N

961 AAAGACAAACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGAT

321 K D K P L G A V A L K S Y E E E L A K D

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1021 CCACGTATTGCCGCCACCATGGAAAACGCCCAGAAAGGTGAAATCATGCCGAACATCCCG
341 P R I A A T M E N A Q K G E I M P N I P

Factor Xa +43 NTR

5 1081 CAGATGTCCGCTTTCTGGTATGCCGTGCTGATCGAAGCCCGCACCTCGGAATCCGACACG
361 Q M S A F W Y A V L I E A R T S E S D T

1141 GCAGGGCCCAACAGCGACCTGGACGTGAACACTGACATTTATTCCAAGGTGCTGGTGACT
381 A G P N S D L D V N T D I Y S K V L V T

10 1201 GCTATATACCTGGCACTCTTCGTGGTGGGCACTGTGGGCAACTCCGTGACAGCCTTCACT
401 A I Y L A L F V V G T V G N S V T A F T

1261 CTAGCGCGGAAGAAGTCACTGCAGAGCCTGCAGAGCACTGTGCATTACCACCTGGGCAGC
15 421 L A R K K S L Q S L Q S T V H Y H L G S

1321 CTGGCACTGTCCGACCTGCTTATCCTTCTGCTGGCCATGCCCCGTGGAGCTATACAACTTC
441 L A L S D L L I L L L A M P V E L Y N F

20 1381 ATCTGGGTACACCATCCCTGGGCCTTTGGGGACGCTGGCTGCCGTGGCTACTATTTCTCTG
461 I W V H H P W A F G D A G C R G Y Y F L

1441 CGTGATGCCTGCACCTATGCCACAGCCCTCAATGTAGCCAGCCTGAGTGTGGAGCGCTAC
481 R D A C T Y A T A L N V A S L S V E R Y

25 1501 TTGGCCATCTGCCATCCCTTCAAGGCCAAGACCCTCATGTCCCGCAGCCGCACCAAGAAA
501 L A I C H P F K A K T L M S R S R T K K

1561 TTCATCAGTGCCATATGGCTAGCTTCGGCGCTGCTGGCTATACCCATGCTTTTCACCATG
30 521 F I S A I W L A S A L L A I P M L F T M

1621 GGCCTGCAGAACCGCAGTGGTGACGGCAGCACCCCTGGCGGCCTGGTGTGCACACCCATT
541 G L Q N R S G D G T H P G G L V C T P I

35 1681 GTGGACACAGCCACTGTCAAGGTCGTATCCAGGTTAACACCTTCATGTCTTCCTGTTTT
561 V D T A T V K V V I Q V N T F M S F L F

1741 CCCATGTTGGTCATCTCCATCCTAAACACCGTGATTGCCAACAACTGACAGTCATGGTG
581 P M L V I S I L N T V I A N K L T V M V

40 1801 CACCAGGCCGCCGAGCAGGGCCGAGTGTGCACCGTGGGCACACACAACGGTTTAGAGCAC
601 H Q A A E Q G R V C T V G T H N G L E H

1861 AGCACGTTCAACATGACCATCGAGCCGGGTCGTGTCCAGGCCCTGCGCCACGGAGTCCTC
45 621 S T F N M T I E P G R V Q A L R H G V L

1921 GTCTTACGTGCTGTGGTCATTGCCTTTGTGGTCTGCTGGCTGCCCTACCACGTGCGACGC
641 V L R A V V I A F V V C W L P Y H V R R

50 1981 CTGATGTTCTGCTATATCTCGGATGAACAGTGGACTACGTTCTCTTCGATTCTACCAC
661 L M F C Y I S D E Q W T T F L F D F Y H

2041 TATTTCTACATGCTAACCAACGCTCTCTTCTACGTGACGCTCCGCCATCAATCCCATCCTC
681 Y F Y M L T N A L F Y V S S A I N P I L

55 2101 TACAACCTGGTCTCCGCCAACTTCCGCCAGGTCTTTCTGTCCACGCTGGCCTGCCTTTGT
701 Y N L V S A N F R Q V F L S T L A C L C

2161 CCTGGGTGGCGCCACCGCCGAAAGAAGAGGCCAACGTTCTCCAGGAAGCCCAACAGCATG
60 721 P G W R H R R K K R P T F S R K P N S M

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2221 TCCAGCAACCATGCCTTTTCCACCAGCGCCACCCGGGAGACCCTGTACgcgccgca
741 S S N H A F S T S A T R E T L Y A A A

5

Flag stop KpnI
GATTATAAAGATGACGATGACAAATAATAAGGTACC
D Y K D D D D K * *

10

SEQ ID NO.: 167

MalE (1-28) Factor Xa NTR (43-424) FLAG

15

SalI +1 MalE leader (1-28)
1 gtcgacATGAAAAATAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTT
1 M K I K T G A R I L A L S A L T T M M F

20

Factor Xa +43 NTR
61 TCCGCCTCGGCTCTCGCCAAAATCATCGAAGCCCGCACCTCGGAATCCGACACGGCAGGG
21 S A S A L A K I I E A R T S E S D T A G

25

121 CCCAACAGCGACCTGGACGTGAACACTGACATTTATTCCAAGGTGCTGGTGACTGCTATA
41 P N S D L D V N T D I Y S K V L V T A I

181 TACCTGGCACTCTTCGTGGTGGGCACTGTGGGCAACTCCGTGACAGCCTTCACTCTAGCG
61 Y L A L F V V G T V G N S V T A F T L A

30

241 CGGAAGAAGTCACTGCAGAGCCTGCAGAGCACTGTGCATTACCACCTGGGCAGCCTGGCA
81 R K K S L Q S L Q S T V H Y H L G S L A

301 CTGTGGACCTGCTTATCCTTCTGCTGGCCATGCCCGTGGAGCTATACAACTTCATCTGG
101 L S D L L I L L L A M P V E L Y N F I W

35

361 GTACACCATCCCTGGGCTTTTGGGACGCTGGCTGCCGTGGCTACTATTTCTGCGTGAT
121 V H H P W A F G D A G C R G Y Y F L R D

40

421 GCCTGCACCTATGCCACAGCCCTCAATGTAGCCAGCCTGAGTGTGGAGCGCTACTTGGCC
141 A C T Y A T A L N V A S L S V E R Y L A

481 ATCTGCCATCCCTTCAAGGCCAAGACCCTCATGTCCCGCAGCCGCACCAAGAAATTCATC
161 I C H P F K A K T L M S R S R T K K F I

45

541 AGTGCCATATGGCTAGCTTCGCGCTGCTGGCTATACCCATGCTTTTACCATGGGCGCTG
181 S A I W L A S A L L A I P M L F T M G L

50

601 CAGAACCGCAGTGGTGACGGCACGCACCCTGGCGGCCTGGTGTGCACACCCATTTGTGGAC
201 Q N R S G D G T H P G G L V C T P I V D

661 ACAGCCACTGTCAAGGTCGTCATCCAGGTAAACACCTTCATGTCCTTCTGTTTCCCATG
221 T A T V K V V I Q V N T F M S F L F P M

55

721 TTGGTCATCTCCATCCTAAACACCGTGATTGCCAACAACCTGACAGTCATGGTGACACCAG
241 L V I S I L N T V I A N K L T V M V H Q

781 GCCGCCGAGCAGGGCCGAGTGTGCACCGTGGGCACACACAACGGTTTTAGAGCACAGCAGC
261 A A E Q G R V C T V G T H N G L E H S T

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841 TTCAACATGACCATCGAGCCGGGTCGTGTCCAGGCCCTGCGCCACGGAGTCCTCGTCTTA
281 F N M T I E P G R V Q A L R H G V L V L

901 CGTGCTGTGGTCATTGCCTTTGTGGTCTGCTGGCTGCCCTACCACGTGCGACGCCTGATG
5 301 R A V V I A F V V C W L P Y H V R R L M

961 TTCTGCTATATCTCGGATGAACAGTGGACTACGTTCTCTTCGATTTCTACCACTATTTTC
321 F C Y I S D E Q W T T F L F D F Y H Y F

10 1021 TACATGCTAACCAACGCTCTCTTCTACGTCAGCTCCGCCATCAATCCCATCCTCTACAAC
341 Y M L T N A L F Y V S S A I N P I L Y N

1081 CTGGTCTCCGCCAACTTCCGCCAGGTCTTTCTGTCCACGCTGGCCTTGCTCTCTGGG
361 L V S A N F R Q V F L S T L A C L C P G

15 1141 TGGCGCCACCGCCGAAAGAAGAGGCCAACGTTCTCCAGGAAGCCCAACAGCATGTCCAGC
381 W R H R R K K R P T F S R K P N S M S S

20 1201 AACCATGCCTTTTTCCACCAGCGCCACCCGGGAGACCCTGTACgcgccgcaGATTATAAA
401 N H A F S T S A T R E T L Y A A A D Y K

NotI Flag

stop KpnI

25 GATGACGATGACAAATAATAAGGTACC
D D D D K

SEQ ID NO.: 169

30 MalE (1-370) Factor Xa NTR (43-424) TrxA (2-109) FLAG

SalI +1 MalE (1-370)

1 GTCGACATGAAAATAAAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTT
1 M K I K T G A R I L A L S A L T T M M F

35 61 TCCGCCTCGGCTCTCGCCAAAATCGAAGAAGGTAAACTGGTAATCTGGATTAACGGCGAT
21 S A S A L A K I E E G K L V I W I N G D

40 121 AAAGGCTATAACGGTCTCGCTGAAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAA
41 K G Y N G L A E V G K K F E K D T G I K

181 GTCACCGTTGAGCATCCGGATAAACTGGAAGAGAAAATTTCCACAGGTTGCGGCAACTGGC
61 V T V E H P D K L E E K F P Q V A A T G

45 241 GATGGCCCTGACATTATCTTCTGGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGC
81 D G P D I I F W A H D R F G G Y A Q S G

301 CTGTTGGCTGAAATCACCCCGGACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGG
101 L L A E I T P D K A F Q D K L Y P F T W

50 361 GATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCG
121 D A V R Y N G K L I A Y P I A V E A L S

421 CTGATTTTATAACAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCG
55 141 L I Y N K D L L P N P P K T W E E I P A

481 CTGGATAAAGAACTGAAAGCGAAAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCG
161 L D K E L K A K G K S A L M F N L Q E P

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Factor Xa +43 NTR

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1741 CCCATGTTGGTCATCTCCATCCTAAACACCGTGATTGCCAACAACTGACAGTCATGGTG
581 P M L V I S I L N T V I A N K L T V M V

5 1801 CACCAGGCCCGGAGCAGGGCCGAGTGTGCACCGTGGGCACACACAACGGTTTAGAGCAC
601 H Q A A E Q G R V C T V G T H N G L E H

1861 AGCACGTTCAACATGACCATCGAGCCGGGTCGTGTCCAGGCCCTGCGCCACGGAGTCCTC
621 S T F N M T I E P G R V Q A L R H G V L

10 1921 GTCTTACGTGCTGTGGTCATTGCCCTTTGTGGTCTGCTGGCTGCCCTACCACGTGCGACGC
641 V L R A V V I A F V V C W L P Y H V R R

1981 CTGATGTTCTGCTATATCTCGGATGAACAGTGGACTACGTTCTCTTCGATTTCTACCAC
15 661 L M F C Y I S D E Q W T T F L F D F Y H

2041 TATTTCTACATGCTAACCAACGCTCTCTTCTACGTCAGCTCCGCCATCAATCCCATCCTC
681 Y F Y M L T N A L F Y V S S A I N P I L

20 2101 TACAACCTGGTCTCCGCCAAGTCCGCCAGGTCTTTCTGTCCACGCTGGCCTGCCTTTGT
701 Y N L V S A N F R Q V F L S T L A C L C

2161 CCTGGGTGGCGCCACCGCGAAAGAAGAGGCCAACGTTCTCCAGGAAGCCCAACAGCATG
721 P G W R H R R K K R P T F S R K P N S M

25

NotI +2

TrxA

2221 TCCAGCAACCATGCCTTTTCCACCAGCGCCACCCGGGAGACCCTGTACGcgggccgcaAGC
741 S S N H A F S T S A T R E T L Y A A A S

30 2281 GATAAAATTATTACCTGACTGACGACAGTTTGTGACACGGATGTACTCAAAGCGGACGGG
761 D K I I H L T D D S F D T D V L K A D G

2341 GCGATCCTCGTCGATTCTGCGGAGAGTGGTGGGTCCGTGCAAAATGATCGCCCCGATT
35 781 A I L V D F W A E W C G P C K M I A P I

2401 CTGGATGAAATCGCTGACGAATATCAGGGCAAAGTACCGTTGCAAACTGAACATCGAT
801 L D E I A D E Y Q G K L T V A K L N I D

40 2461 CAAAACCTGGCACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTGCTGTTT
821 Q N P G T A P K Y G I R G I P T L L L F

2521 AAAACCGGTGAAGTGGCGGCAACCAAGTGGGTGCACTGTCTAAAGGTGAGTTGAAAGAG
841 K N G E V A A T K V G A L S K G Q L K E

45

NotI +2 Flag stop

2581 TTCCTCGACGCTAACCTGGCGcgggccgcaGATTATAAAGATGACGATGACAAATAATAA
861 F L D A N L A A A A D Y K D D D D K * *

50

KpnI

2641 GGTACC

55

SEQ ID NO.: 170

MalE (1-28) Factor Xa NTR (43-424) TrxA (2-109) FLAG

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Sali +1 Male leader (1-28)
1 gtcgacATGAAAATAAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTT
1 M K I K T G A R I L A L S A L T T M M F

5 Factor Xa +43 NTR
61 TCCGCCTCGGCTCTCGCCAAAATCATCGAAGCCCGCACCTCGGAATCCGACACGGCAGGG
21 S A S A L A K I I E A R T S E S D T A G

10 121 CCCAACAGCGACCTGGACGTGAACACTGACATTATTCCAAGGTGCTGGTGA CTGCTATA
41 P N S D L D V N T D I Y S K V L V T A I

15 181 TACCTGGCACTCTTCGTGGTGGGCACTGTGGGCAACTCCGTGACAGCCTTCACTCTAGCG
61 Y L A L F V V G T V G N S V T A F T L A

20 241 CGGAAGAAGTCACTGCAGAGCCTGCAGAGCACTGTGCATTACCACCTGGGCAGCCTGGCA
81 R K K S L Q S L Q S T V H Y H L G S L A

25 301 CTGTGGACCTGCTTATCCTTCTGCTGGCCATGCCCGTGGAGCTATACA ACTTCACTCTGG
101 L S D L L I L L L A M P V E L Y N F I W

361 GTACACCATCCCTGGGCTTTGGGGACGCTGGCTGCCGTGGCTACTATTTCTGCGTGAT
121 V H H P W A F G D A G C R G Y Y F L R D

421 GCCTGCACCTATGCCACAGCCCTCAATGTAGCCAGCCTGAGTGTGGAGCGCTACTTGGCC
141 A C T Y A T A L N V A S L S V E R Y L A

481 ATCTGCCATCCCTTCAAGGCCAAGACCCTCATGTCCGCAGCCGCACCAAGAAATTCATC
161 I C H P F K A K T L M S R S R T K K F I

30 541 AGTGCCATATGGCTAGCTTCGGCGCTGCTGGCTATACCCATGCTTTTCCACATGGGCCTG
181 S A I W L A S A L L A I P M L F T M G L

601 CAGAACCGCAGTGGTGACGGCACGCACCCTGGCGGCCTGGTGTGCACACCCATTGTGGAC
201 Q N R S G D G T H P G G L V C T P I V D

35 661 ACAGCCACTGTCAAGGTCGTATCCAGGTTAACACCTTCATGTCCTTCTGTTTCCCATG
221 T A T V K V V I Q V N T F M S F L F P M

721 TTGGTCATCTCCATCCTAAACACCGTGATTGCCAACA AACTGACAGTCATGGTGCACCAG
241 L V I S I L N T V I A N K L T V M V H Q

781 GCCGCCGAGCAGGGCCGAGTGTGCACCGTGGGCACACACAACGGTTTAGAGCACAGCACG
261 A A E Q G R V C T V G T H N G L E H S T

45 841 TTCAACATGACCATCGAGCCGGGTCGTGTCCAGGCCCTGCGCCACGGAGTCTCTCGTCTTA
281 F N M T I E P G R V Q A L R H G V L V L

901 CGTGCTGTGGTCATTGCCTTTGTGGTCTGCTGGCTGCCCTACCACGTGCGACGCCTGATG
301 R A V V I A F V V C W L P Y H V R R L M

50 961 TTCTGCTATATCTCGGATGAACAGTGGACTACGTTCTCTTCGATTCTTACCACTATTTC
321 F C Y I S D E Q W T T F L F D F Y H Y F

1021 TACATGCTAACCAACGCTCTCTTCTACGTCAGCTCCGCCATCAATCCCATCCTCTACAAC
341 Y M L T N A L F Y V S S A I N P I L Y N

1081 CTGGTCTCCGCCAACTTCCGCCAGGTCTTTCTGTCCACGCTGGCCTGCCTTTGTCTCTGGG
361 L V S A N F R Q V F L S T L A C L C P G

60 1141 TGGCGCCACCGCCGAAAGAAGAGGCCAACGTTCTCCAGGAAGCCCAACAGCATGTCCAGC

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381 W R H R R K K R P T F S R K P N S M S S

NotI +2 TrxA

5 1201 AACCATGCCTTTTCCACCAGCGCCACCCGGGAGACCCTGTACgcgccgcaAGCGATAAA

401 N H A F S T S A T R E T L Y A A A S D K

1261 ATTATTACCTGACTGACGACAGTTTTGACACGGATGTACTCAAAGCGGACGGGGCGATC

421 I I H L T D D S F D T D V L K A D G A I

10 1321 CTCGTCGATTTCTGGGCAGAGTGGTGCGGTCCGTGCAAAATGATCGCCCCGATTCTGGAT

441 L V D F W A E W C G P C K M I A P I L D

1381 GAAATCGCTGACGAATATCAGGGCAAAC TGACCGTTGCAAACTGAACATCGATCAAAAC

461 E I A D E Y Q G K L T V A K L N I D Q N

15 1441 CCTGGCACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTGCTGTTCAAAAAC

481 P G T A P K Y G I R G I P T L L L F K N

1501 GGTGAAGTGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTGAAAGAGTTCCTC

20 501 G E V A A T K V G A L S K G Q L K E F L

NotI Flag stop KpnI

1561 GACGCTAACCTGGCAGcgcccgcaGATTATAAAGATGACGATGACAAATAATAAGGTACC

25 521 D A N L A A A A D Y K D D D D K

SEQ ID NO.: 188

30 Human β 2AR GS1 α chimeric fusion

SalI +1 B2AR

1 GTCGACATGG GGCAACCCGG GAACGGCAGC GCCTTCTTGC TGGCACCCAA

TGGAAGCCAT

35 61 GCGCCGGACC ACGACGTCAC GCAGCAAAGG GACGAGGTGT GGGTGGTGGG

CATGGGCATC

121 GTCATGTCTC TCATCGTCCT GGCCATCGTG TTTGGCAATG TGCTGGTCAT

CACAGCCATT

40 181 GCCAAGTTCG AGCGTCTGCA GACGGTCACC AACTACTTCA TCACTTCACT

GGCCTGTGCT

241 GATCTGGTCA TGGGCCTAGC AGTGGTGCCC TTTGGGGCCG CCCATATTCT

TATGAAAATG

301 TGGACTTTTG GCAACTTCTG GTGCGAGTTT TGGACTTCCA TTGATGTGCT

45 GTGCGTCACG

361 GCCAGCATTG AGACCCTGTG CGTGATCGCA GTGGATCGCT ACTTTGCCAT

TACTTCACCT

421 TTCAAGTACC AGAGCCTGCT GACCAAGAAT AAGGCCCGGG TGATCATTCT

GATGGTGTGG

50 481 ATTGTGTGAG GCCTTAYCTC CTTCTTGCCC ATTGAGATGC ACTGGTACAG

GGCCACCCAC

541 CAGGAAGCCA TCAACTGCTA TGCCAATGAG ACCTGCTGTG ACTTCTTCAC

GAACCAAGCC

601 TATGCCATTG CCTCTTCCAT CGTGTCCCTT TACGTTCCCC TGGTGATCAT

55 GGTCTTCGTC

661 TACTCCAGGG TCTTTCAGGA GGCCAAAAGG CAGCTCCAGA AGATTGACAA

ATCTGAGGGC

721 CGCTTCCATG TCCAGAACCT TAGCCAGGTG GAGCAGGATG GCGGACGGG

GCATGGACTC

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781 CGCAGATCTT CCAAGTTCTG CTTGAAGGAG CACAAAGCCC TCAAGACGTT
AGGCATCATC
841 ATGGGCACTT TCACCCTCTG CTGGCTGCCC TTCTTCATCG TTAACATTGT
GCATGTGATC
5 901 CAGGATAACC TCATCCGTAA GGAAGTTTAC ATCCTCCTAA ATTGGATAGG
CTATGTCAAT
961 TCTGGTTTCA ATCCCCTTAT CTA CTACTGCCGG AGCCCAGATT TCAGGATTGC
CTTCCAGGAG
1021 CTTCTGTGCC TGC GCAGGTC TTCTTTGAAG GCCTATGGCA ATGGCTACTC
10 CAGCAACGGC
1081 AACACAGGGG AGCAGAGTGG ATATCACGTG GAACAGGAGA AAGAAAATAA
ACTGCTGTGT
1141 GAAGACCTCC CAGGCACGGA AGACTTTGTG GGCCATCAAG GTACTGTGCC
TAGCGATAAC
15
Last B2AR Linker
sequence
1201 ATTGATTAC AAGGGAGGAA TTGTAGTACA AATGACTCAC TGCTAGAGCG
TGGCCAGACG
20
PstI XhoI +2 GS1 alpha
1261 GTCACCAACC TGCAGCTCGA GGGCTGCCTC GGGAACAGTA AGACCGAGGA
CCAGCGCAAC
25
1321 GAGGAGAAGG CGCAGCGTGA GGCCAACAAA AAGATCGAGA AGCAGCTGCA
GAAGGACAAG
1381 CAGGTCTACC GGGCCACGCA CCGCCTGCTG CTGCTGGGTG CTGGAGAATC
TGGTAAAAGC
30 1441 ACCATTGTGA AGCAGATGAG GATCCTGCAT GTTAATGGGT TTAATGGAGA
CAGTGAGAAG
1501 GCAACCAAAG TGCAGGACAT CAAAAACAAC CTGAAAGAGG CGATTGAAAC
CATTGTGGCC
1561 GCCATGAGCA ACCTGGTGCC CCCC GTGGAG CTGGCCAACC CCGAGAACCA
35 GTTCAGAGTG
1621 GACTACATCC TGAGTGTGAT GAACGTGCCT GACTTTGACT TCCCTCCCGA
ATTCTATGAG
1681 CATGCCAAGG CTCTGTGGGA GGATGAAGGA GTGCGTGCCT GCTACGAACG
CTCCAACGAG
40 1741 TACCAGCTGA TTGACTGTGC CCAGTACTTC CTGGACAAGA TCGACGTGAT
CAAGCAGGCT
1801 GACTATGTGC CGAGCGATCA GGACCTGCTT CGCTGCCGTG TCCTGACTTC
TGGAATCTTT
1861 GAGACCAAGT TCCAGGTGGA CAAAGTCAAC TTCCACATGT TTGACGTGGG
45 TGGCCAGCGC
1921 GATGAACGCC GCAAGTGGAT CCAGTGCTTC AACGATGTGA CTGCCATCAT
CTTCGTGGTG
1981 GCCAGCAGCA GCTACAACAT GGT CATCCGG GAGGACAACC AGACCAACCG
CCTGCAGGAG
50 2041 GCTCTGAACC TCTTCAAGAG CATCTGGAAC AACAGATGGC TGCGCACCAT
CTCTGTGATC
2101 CTGTTCTCTCA ACAAGCAAGA TCTGCTCGCT GAGAAAGTCC TTGCTGGGAA
ATCGAAGATT
2161 GAGGACTACT TTCCAGAATT TGCTCGCTAC ACTACTCCTG AGGATGCTAC
55 TCCCAGAGCCC
2221 GGAGAGGACC CACGCGTGAC CCGGGCCAAG TACTTCATTC GAGATGAGTT
TCTGAGGATC
2281 AGCACTGCCA GTGGAGATGG GCGTCACTAC TGCTACCCTC ATTTACCTG
CGCTGTGGAC

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2341 ACTGAGAACAA TCCGCCGTGT GTTCAACGAC TGCCGTGACA TCATTCAGCG
CATGCACCTT

5 2401 CGTCAGTACG AGCTGCTCAT CGATTAATAA TCTAGAGGAT CCCCGCGCCC
TCATCCGAAA

2461 GGGCG

10

SEQ ID NO.: 190

Human β 2AR stop GS1 α transcriptional fusion

15 PstI +1 B2AR

1 GTCGACATGG GGCAACCCGG GAACGGCAGC GCCTTCTTGC TGGCACCCAA
TGGAAGCCAT

20

61 GCGCCGGACC ACGACGTCAC GCAGCAAAGG GACGAGGTGT GGGTGGTGGG
CATGGGCATC

121 GTCATGTCTC TCATCGTCCT GGCCATCGTG TTGGGCAATG TGCTGGTCAT
CACAGCCATT

25 181 GCCAAGTTCT AGCGTCTGCA GACGGTCACC AACTACTTCA TCACTTCACT
GGCCTGTGCT

241 GATCTGGTCA TGGGCCTAGC AGTGGTGCCC TTGGGGCCG CCCATATTCT
TATGAAAATG

301 TGGACTTTTG GCAACTTCTG GTGCGAGTTT TGGACTTCCA TTGATGTGCT

30 GTGCGTCACG

361 GCCAGCATTG AGACCCTGTG CGTGATCGCA GTGGATCGCT ACTTTGCCAT
TACTTCACCT

421 TTCAAGTACC AGAGCCTGCT GACCAAGAAT AAGGCCCCGG TGATCAITCT
GATGGTGTGG

35 481 ATTGTGTGAG GCCTTAYCTC CTTCTTGCCC ATTCAGATGC ACTGGTACAG
GGCCACCCAC

541 CAGGAAGCCA TCAACTGCTA TGCCAATGAG ACCTGCTGTG ACTTCTTCAC
GAACCAAGCC

601 TATGCCATTG CCTCTTCCAT CGTGTCTTTC TACGTTCCCC TGGTGATCAT

40 GGTCTTCGTC

661 TACTCCAGGG TCTTTCAGGA GGCCAAAAGG CAGCTCCAGA AGATTGACAA
ATCTGAGGGC

721 CGCTTCCATG TCCAGAACCT TAGCCAGGTG GAGCAGGATG GGCGGACGGG
GCATGGACTC

45 781 CGCAGATCTT CCAAGTTCTG CTTGAAGGAG CACAAAGCCC TCAAGACGTT
AGGCATCATC

841 ATGGGCACTT TCACCCTCTG CTGGCTGCCC TTCTTCATCG TTAACATTGT
GCATGTGATC

901 CAGGATAACC TCATCCGTAA GGAAGTTTAC ATCCTCCTAA ATTGGATAGG

50 CTATGTCAAT

961 TCTGGTTTCA ATCCCCTTAT CTA CTGCTGCGG AGCCAGATT TCAGGATTGC
CTTCCAGGAG

1021 CTTCTGTGCC TGCGCAGGTC TTCTTTGAAG GCCTATGGCA ATGGCTACTC
CAGCAACGGC

55 1081 AACACAGGGG AGCAGAGTGG ATATCACGTG GAACAGGAGA AAGAAAATAA
ACTGCTGTGT

1141 GAAGACCTCC CAGGCACGGA AGACTTTGTG GGCCATCAAG GTACTGTGCC
TAGCGATAAC

WO 03/072014

PCT/US02/16877

Last B2AR Linker

sequence
1201 ATTGATTAC AAGGGAGGAA TTGTAGTACA AATGACTCAC TGCTAGAGCG
TGGCCAGACG

5

PstI Stop SD XhoI +2 GS1 alpha

1261 GTCACCAACC TGCAGTAATA ATCAAGGAGG CCCTCGAGAT GGGCTGCCTC
GGGAACAGTA

10

1321 AGACCGAGGA CCAGCGCAAC GAGGAGAAGG CGCAGCGTGA GGCCAACAAA
AAGATCGAGA
1381 AGCAGCTGCA GAAGGACAAG CAGGTCTACC GGGCCACGCA CCGCCTGCTG
CTGCTGGGTG

15

1441 CTGGAGAATC TGGTAAAAGC ACCATTGTGA AGCAGATGAG GATCCTGCAT
GTTAATGGGT
1501 TTAATGGAGA CAGTGAGAAG GCAACCAAAG TGCAGGACAT CAAAAACAAC
CTGAAAGAGG
1561 CGATTGAAAC CATTGTGGCC GCCATGAGCA ACCTGGTGCC CCCCCTGGAG

20

CTGGCCAACC
1621 CCGAGAACCA GTTCAGAGTG GACTACATCC TGAGTGTGAT GAACGTGCCT
GACTTTGACT
1681 TCCCTCCCGA ATTCTATGAG CATGCCAAGG CTCTGTGGGA GGATGAAGGA
GTGCGTGCCT

25

1741 GCTACGAACG CTCCAACGAG TACCAGCTGA TTGACTGTGC CCAGTACTTC
CTGGACAAGA
1801 TCGACGTGAT CAAGCAGGCT GACTATGTGC CGAGCGATCA GGACCTGCTT
CGCTGCCGTG
1861 TCCTGACTTC TGAATCTTT GAGACCAAGT TCCAGGTGGA CAAAGTCAAC

30

TTCCACATGT
1921 TTGACGTGGG TGGCCAGCGC GATGAACGCC GCAAGTGGAT CCAGTGCTTC
AACGATGTGA
1981 CTGCCATCAT CTTCTGTGGT GCCAGCAGCA GCTACAACAT GGTCAATCCG
GAGGACAACC

35

2041 AGACCAACCG CCTGCAGGAG GCTCTGAACC TCTTCAAGAG CATCTGGAAC
AACAGATGGC
2101 TGCGCACCAT CTCTGTGATC CTGTTCTCTA ACAAGCAAGA TCTGCTCGCT
GAGAAAGTCC
2161 TTGCTGGGAA ATCGAAGATT GAGGACTACT TTCCAGAATT TGCTCGCTAC

40

ACTACTCCTG
2221 AGGATGCTAC TCCCGAGCCC GGAGAGGACC CACGCGTGAC CCGGGCCAAG
TACTTCATTC
2281 GAGATGAGTT TCTGAGGATC AGCACTGCCA GTGGAGATGG GCGTCACTAC
TGCTACCCTC

45

2341 ATTTCACCTG CGCTGTGGAC ACTGAGAACA TCCGCCGTGT GTTCAACGAC
TGCCGTGACA

ClaI Stop XbaI

50

2401 TCATTGAGCG CATGCACCTT CGTCAGTACG AGCTGCTCAT CGATTAATAA
TCTAGAGGAT

Stem-loop

2461 CCCCGCGCCC TCATCCGAAA GGGCG

55

SEQ ID NO.: 192

Human GS1 α

WO 03/072014

PCT/US02/16877

XhoI

1
CTCGAGATGGGCTGCCTCGGGAACAGTAAGACCGAGGACCAGCGCAACGAGGAGAAGGCGCAGCGT

5 1 M G C L G N S K T E D Q R N E E K A Q R

61 GAGGCCAACAAAAAGATCGAGAAGCAGCTGCAGAAGGACAAGCAGGTCTACCGGGCCACG

21 E A N K K I E K Q L Q K D K Q V Y R A T

10 121 CACCGCCTGCTGCTGCTGGGTGCTGGAGAATCTGGTAAAAGCACCATTGTGAAGCAGATG

41 H R L L L L G A G E S G K S T I V K Q M

181 AGGATCCTGCATGTTAATGGGTTTAAATGGAGACAGTGAGAAGGCAACCAAAGTGCAGGAC

61 R I L H V N G F N G D S E K A T K V Q D

15 241 ATCAAAAACAACCTGAAAAGAGGCGATTGAAACCATTGTGGCCGCCATGAGCAACCTGGTG

81 I K N N L K E A I E T I V A A M S N L V

301 CCCCCGTGGAGCTGGCCAACCCCCGAGAACCAGTTCAGAGTGGACTACATCCTGAGTGTG

20 101 P P V E L A N P E N Q F R V D Y I L S V

361 ATGAACGTGCCTGACTTTGACTTCCCTCCCGAATTCTATGAGCATGCCAAGGCTCTGTGG

121 M N V P D F D F P P E F Y E H A K A L W

25 421 GAGGATGAAGGAGTGGTGCCTGCTACGAACGCTCCAACGAGTACCAGCTGATTGACTGT

141 E D E G V R A C Y E R S N E Y Q L I D C

481 GCCCAGTACTTCTGGACAAGATCGACGTGATCAAGCAGGCTGACTATGTGCCGAGCGAT

161 A Q Y F L D K I D V I K Q A D Y V P S D

30 541 CAGGACCTGCTTCGCTGCCGTGCTGCTGACTTCTGGAATCTTTGAGACCAAGTTCCAGGTG

181 Q D L L R C R V L T S G I F E T K F Q V

601 GACAAAGTCAACTTCCACATGTTTGACGTGGGTGGCCAGCGCGATGAACGCCGCAAGTGG

35 201 D K V N F H M F D V G G Q R D E R R K W

661 ATCCAGTGCTTCAACGATGTGACTGCCATCATCTTCGTGGTGGCCAGCAGCAGCTACAAC

221 I Q C F N D V T A I I F V V A S S S Y N

40 721 ATGGTCATCCGGGAGGACAACCAGACCAACCGCCTGCAGGAGGCTCTGAACCTCTTCAAG

241 M V I R E D N Q T N R L Q E A L N L F K

781 AGCATCTGGAACAACAGATGGCTGCGCACCATCTCTGTGATCCTGTTCTCAACAAGCAA

261 S I W N N R W L R T I S V I L F L N K Q

45 841 GATCTGCTCGCTGAGAAAGTCTTGTCTGGGAAATCGAAGATTGAGGACTACTTTCCAGAA

281 D L L A E K V L A G K S K I E D Y F P E

901 TTTGCTCGCTACACTACTCCTGAGGATGCTACTCCCGAGCCCGGAGAGGACCCACGCGTG

50 301 F A R Y T T P E D A T P E P G E D P R V

961 ACCCGGGCCAAGTACTTTCATTTCGAGATGAGTTTCTGAGGATCAGCACTGCCAGTGGAGAT

321 T R A K Y F I R D E F L R I S T A S G D

55 1021 GGGCGTCACTACTGCTACCCTCATTTACCTGCGCTGTGGACACTGAGAACATCCGCCGT

341 G R H Y C Y P H F T C A V D T E N I R R

1081 GTGTTCAACGACTGCCGTGACATCATTCAGCGCATGCACCTTCGTGAGTACGAGCTGCTC

361 V F N D C R D I I Q R M H L R Q Y E L L

60

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ClaI
ATCGAT

5 SEQ ID NO.: 193

Human GS2 α

XhoI

10 1 CTCGAGATGGGCTGCCTCGGGAACAGTAAGACCGAGGACCAGCGCAACGAGGAGAAGGCGCAGCGT
1 M G C L G N S K T E D Q R N E E K A Q R

61 GAGGCCAACAAAAAGATCGAGAAGCAGCTGCAGAAGGACAAGCAGGTCTACCGGGCCACG
21 E A N K K I E K Q L Q K D K Q V Y R A T

15 121 CACCGCCTGCTGCTGCTGGGTGCTGGAGAATCTGGTAAAAGCACCATTGTGAAGCAGATG
41 H R L L L L G A G E S G K S T I V K Q M

181 AGGATCCTGCATGTTAATGGGTTTAAATGGAGAGGGCGGCGAAGAGGACCCGAGGCTGCA
20 61 R I L H V N G F N G E G G E E D P Q A A

241 AGGAGCAACAGCGATGGTGAGAAGGCAACCAAAGTGCAGGACATCAAAAACAACCTGAAA
81 R S N S D G E K A T K V Q D I K N N L K

25 301 GAGGCGATTGAAACCATTGTGGCCGCCATGAGCAACCTGGTGGCCCCCGTGGAGCTGGCC
101 E A I E T I V A A M S N L V P P V E L A

361 AACCCCGAGAACCAGTTCAGAGTGGACTACATCCTGAGTGTGATGAACGTGCCTGACTTT
121 N P E N Q F R V D Y I L S V M N V P D F

30 421 GACTTCCCTCCCGAATTCTATGAGCATGCCAAGGCTCTGTGGGAGGATGAAGGAGTGCCT
141 D F P P E F Y E H A K A L W E D E G V R

481 GCCTGCTACGAACGCTCCAACGAGTACCAGCTGATTGACTGTGCCCAGTACTTCCTGGAC
35 161 A C Y E R S N E Y Q L I D C A Q Y F L D

541 AAGATCGACGTGATCAAGCAGGCTGACTATGTGCCGAGCGATCAGGACCTGCTTCGCTGC
181 K I D V I K Q A D Y V P S D Q D L L R C

40 601 CGTGTCTGACTTCTGGAATCTTTGAGACCAAGTTCCAGGTGGACAAAGTCAACTTCCAC
201 R V L T S G I F E T K F Q V D K V N F H

661 ATGTTTGACGTGGGTGGCCAGCGCGATGAACGCCGCAAGTGGATCCAGTGCTTCAACGAT
221 M F D V G G Q R D E R R K W I Q C F N D

45 721 GTGACTGCCATCATCTTCGTGGTGGCCAGCAGCAGCTACAACATGGTCATCCGGGAGGAC
241 V T A I I F V V A S S S Y N M V I R E D

781 AACCAGACCAACCGCCTGCAGGAGGCTCTGAACCTCTTCAAGAGCATCTGGAACAACAGA
50 261 N Q T N R L Q E A L N L F K S I W N N R

841 TGGCTGCGCACCATCTCTGTGATCCTGTTTCCTCAACAAGCAAGATCTGCTCGCTGAGAAA
281 W L R T I S V I L F L N K Q D L L A E K

55 901 GTCCTTGCTGGGAAATCGAAGATTGAGGACTACTTTCAGAATTTGCTCGCTACACTACT
301 V L A G K S K I E D Y F P E F A R Y T T

961 CCTGAGGATGCTACTCCCGAGCCCGGAGAGGACCCACGCGTGACCCGGGCCAAGTACTTC
321 P E D A T P E P G E D P R V T R A K Y F

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1021 ATTCGAGATGAGTTTCTGAGGATCAGCACTGCCAGTGGAGATGGGCGTCACTACTGCTAC
341 I R D E F L R I S T A S G D G R H Y C Y

5 1081 CCTCATTTACCTGCGCTGTGGACACTGAGAACATCCGCCGTGTGTTCAACGACTGCCGT
361 P H F T C A V D T E N I R R V F N D C R

1141 GACATCATTCAGCGCATGCACCTTCGTACGTACGAGCTGCTCATCGAT
381 D I I Q R M H L R Q Y E L L

ClaI

SEQ ID NO.: 194

15

Human Gαq

XhoI
1 CTCGAGATGACTCTGGAGTCCATCATGGCGTGCTGCCTGAGCGAGGAGGCCAAGGAAGCCCGGCGG
20 1 M T L E S I M A C C L S E E A K E A R R

61 ATCAACGACGAGATCGAGCGGCAGCTCCGCAGGGACAAGCGGGACGCCCCGGGAGCTC
21 I N D E I E R Q L R R D K R D A R R E L

121 AAGCTGCTGCTGCTCGGGACAGGAGAGTGGCAAGAGTACGTTTATCAAGCAGATGAGA
41 K L L L L G T G E S G K S T F I K Q M R

181 ATCATCCATGGGTCAGGATACTCTGATGAAGATAAAAGGGGCTTCACCAAGCTGGTGAT
61 I I H G S G Y S D E D K R G F T K L V Y

241 CAGAACATCTTCACGGCCATGCAGGCCATGATCAGAGCCATGGACACACTCAAGATCCCA
81 Q N I F T A M Q A M I R A M D T L K I P

301 TACAAGTATGAGCACAATAAGGCTCATGCACAATTAGTTCGAGAAGTTGATGTGGAGAAG
101 Y K Y E H N K A H A Q L V R E V D V E K

361 GTGTCTGCTTTTGAGAATCCATATGTAGATGCAATAAAGAGTTTATGGAATGATCCTGGA
121 V S A F E N P Y V D A I K S L W N D P G

421 ATCCAGGAATGCTATGATAGACGACGAGAATATCAATTATCTGACTCTACCAAATACTAT
141 I Q E C Y D R R R E Y Q L S D S T K Y Y

481 CTTAATGACTTGGACCGCGTAGCTGACCCTGCCTACCTGCCTACGCAACAAGATGTGCTT
161 L N D L D R V A D P A Y L P T Q Q D V L

541 AGAGTTCGAGTCCCCACCACAGGGATCATCGAATAACCCCTTTGACTTACAAAGTGTCAAT
181 R V R V P T T G I I E Y P F D L Q S V I

601 TTCAGAATGGTCGATGTAGGGGGCCAAAGGTCAGAGAGAAGAAAATGGATACACTGCTTT
201 F R M V D V G G Q R S E R R K W I H C F

661 GAAAATGTCACCTCTATCATGTTTCTAGTAGCGCTTAGTGAATATGATCAAGTTCTCGTG
221 E N V T S I M F L V A L S E Y D Q V L V

721 GAGTCAGACAATGAGAACCGAATGGAGGAAAGCAAGGCTCTCTTTAGAACAATTATCACA
241 E S D N E N R M E E S K A L F R T I I T

781 TACCCCTGGTTCCAGAACTCCTCGGTTATTCTGTTCTTAAACAAGAAAGATCTTCTAGAG
261 Y P W F Q N S S V I L F L N K K D L L E

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841 GAGAAAATCATGTATTCCCATCTAGTCGACTACTTCCCAGAATATGATGGACCCAGAGA
281 E K I M Y S H L V D Y F P E Y D G P Q R

5 901 GATGCCCAGGCAGCCCGAGAATTCATTCTGAAGATGTTCTGCGTGGACCTGAACCCAGACAGT
301 D A Q A A R E F I L K M F V D L N P D S

961 GACAAAATTATCTACTCCCACTTCACGTGCGCCACAGACACCGAGAATATCCGCTTTGTC
321 D K I I Y S H F T C A T D T E N I R F V

10

Clal
1021
TTTGCTGCCGTCAAGGACACCATCCTCCAGTTGAACCTGAAGGAGTACAATCTGGTCATCGAT

15 341 F A A V K D T I L Q L N L K E Y N L V

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20

Human Gio.

XhoI

1 CTCGAGATGGGCTGCACCGTGAGCGCCGAGGACAAGGCGGCGGCCGAGCGCTCTAAGATGATCGAC
25 1 M G C T V S A E D K A A A E R S K M I D

61 AAGAACCTGCGGGAGGACGGAGAGAAGGCGGCGGGAGGTGAAGTTGCTGCTGTTGGGT
21 K N L R E D G E K A A R E V K L L L L G

30 121 GCTGGGGAGTCAGGGAAGAGCACCATCGTCAAGCAGATGAAGATCATCCACGAGGATGGC
41 A G E S G K S T I V K Q M K I I H E D G

181 TACTCCGAGGAGGAATGCCGGCAGTACCGGGCGGTTGTCTACAGCAACACCATCCAGTCC
61 Y S E E E C R Q Y R A V V Y S N T I Q S

35 241 ATCATGGCCATTGTCAAAGCCATGGGAAACCTGCAGATCGACTTTGCCGACCCCTCCAGA
81 I M A I V K A M G N L Q I D F A D P S R

301 GCGGACGACGCCAGGCAGCTATTTGCACTGTCCTGCACCGCCGAGGAGCAAGGCGTGCTC
40 101 A D D A R Q L F A L S C T A E E Q G V L

361 CCTGATGACCTGTCCGGCGTCATCCGGAGGCTCTGGGCTGACCATGGTGTGCAGGCCTGC
121 P D D L S G V I R R L W A D H G V Q A C

45 421 TTTGGCCGCTCAAGGAATACCAGCTCAACGACTCAGCTGCCTACTACCTGAACGACCTG
141 F G R S R E Y Q L N D S A A Y Y L N D L

481 GAGCGTATTGCACAGAGTGA CTACATCCCCACACAGCAAGATGTGCTACGGACCCGCGTA
61 E R I A Q S D Y I P T Q Q D V L R T R V

50 541 AAGACCACGGGGATCGTGAGACACACTTCACCTTCAAGGACCTACACTTCAAGATGTTT
181 K T T G I V E T H F T F K D L H F K M F

601 GATGTGGGTGGTCAGCGGTCTGAGCGGAAGAAGTGGATCCACTGCTTTGAGGGCGTCACA
55 201 D V G G Q R S E R K K W I H C F E G V T

661 GCCATCATCTTCTGCGTAGCCTTGAGCGCCTATGACTTGGTGCTAGCTGAGGACGAGGAG
221 A I I F C V A L S A Y D L V L A E D E E

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721 ATGAACCGCATGCATGAGAGCATGAAGCTATTTCGATAGCATCTGCAACAACAAGTGGTTC
241 M N R M H E S M K L F D S I C N N K W F

5 781 ACAGACACGTCCATCATCCTCTTCTCAACAAGAAGGACCTGTTTGAGGAGAAGATCACA
261 T D T S I I L F L N K K D L F E E K I T

841 CACAGTCCCCTGACCATCTGCTTCCCTGAGTACACAGGGGCCAACAAATATGATGAGGCA
281 H S P L T I C F P E Y T G A N K Y D E A

10 901 GCCAGCTACATCCAGAGTAAGTTTGAGGACCTGAATAAGCGCAAAGACACCAAGGAGATC
301 A S Y I Q S K F E D L N K R K D T T K E I

961 TACACGCACTTCACGTGCGCCACCGACACCAAGAACGTGCAGTTCTGTGTTGACGCCGTC
321 Y T H F T C A T D T K N V Q F V F D A V

15

1021 ACCGATGTCATCATCAAGAACAACCTGAAGGACTGCGGCCTCTTTCATGCAT
341 T D V I I K N N L K D C G L F

ClaI

20

SEQ ID NO.: 196

Human Gα12/13

25

XhoI

1 CTCGAGATGTCCGGGGTGGTGCGGACCCTCAGCCGCTGCCTGCTGCCGGCCGAGGCCGGCGGGGCC
1 M S G V V R T L S R C L L P A E A G G A

30 61 CGCGAGCGCAGGGCGGGCAGCGGCGCGCGACGCGGAGCGCGAGGCCCGGAGGCGTAGC
21 R E R R A G S G A R D A E R E A R R S

121 CGCGACATCGACGCGCTGCTGGCCCGCGAGCGGCGCGGTCCGGCGCCTGGTGAAGATC
41 R D I D A L L A R E R R A V R R L V K I

35 181 CTGCTGCTGGGCGCGGGCGAGAGCGGCAAGTCCACGTTCCCTCAAGCAGATGCGCATCATC
61 L L L G A G E S G K S T F L K Q M R I I

241 CACGGCCGCGAGTTCCGACCAGAAGGCGCTGCTGGAGTTCCGCGACACCATCTTCGACAAC
40 81 H G R E F D Q K A L L E F R D T I F D N

301 ATCCTCAAGGGCTCAAGGGTTCTTGTGATGCACGAGATAAGCTTGGCATTCCTTGGCAG
101 I L K G S R V L V D A R D K L G I P W Q

45 361 TATTCTGAAAATGAGAAGCATGGGATGTTCTGATGGCCTTCGAGAACAAGCGGGGCTG
121 Y S E N E K H G M F L M A F E N K A G L

421 CCTGTGGAGCCGGCCACCTTCCAGCTGTACGTCCCGGCCCTGAGCGCACTCTGGAGGGAT
141 P V E P A T F Q L Y V P A L S A L W R D

50 481 TCTGGCATCAGGGAGGCTTTTCAGCCGAGAGCGAGTTTCAGCTGGGGGAGTCGGTGAAG
161 S G I R E A F S R R S E F Q L G E S V K

541 TACTTCTGGACAACCTTGGACCGGATCGGCCAGCTGAATTACTTTCCTAGTAAGCAAGAT
55 181 Y F L D N L D R I G Q L N Y F P S K Q D

601 ATCCTGCTGGCTAGGAAAGCCACCAAGGAATTGTGGAGCATGACTTCGTTATTAAGAAG
201 I L L A R K A T K G I V E H D F V I K K

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661 ATCCCCTTTAAGATGGTGGATGTGGGCGGCCAGCGGTCCCAGCGCCAGAAGTGGTTCCAG
221 I P F K M V D V G G Q R S Q R Q K W F Q

721 TGCTTCGACGGGATCACGTCCATCCTGTTTCATGGTCTCCTCCAGCGAGTACGACCAGGTC
5 241 C F D G I T S I L F M V S S S E Y D Q V

781 CTCATGGAGGACAGGCGCACCAACCGGCTGGTGGAGTCCATGAACATCTTCGAGACCATC
261 L M E D R R T N R L V E S M N I F E T I

10 841 GTCAACAACAAGCTCTTCTTCAACGTCTCCATCATTCTCTTCTCAACAAGATGGACCTC
281 V N N K L F F N V S I I L F L N K M D L

901 CTGGTGGAGAAGGTGAAGACCGTGAGCATCAAGAAGCACTTCCCGGACTTCAGGGGCGAC
301 L V E K V K T V S I K K H F P D F R G D

15 961 CCGCACCAGCTGGAGGACGTCCAGCGCTACCTGGTCCAGTGCTTCGACAGGAAGAGACGG
321 P H Q L E D V Q R Y L V Q C F D R K R R

1021 AACCGCAGCAAGCCACTCTTCCACCACTTCACCACCGCCATCGACACCGAGAACGTCCGC
20 341 N R S K P L F H H F T T A I D T E N V R

1081 TTCGTGTTCCATGCTGTGAAAGACACCATCCTGCAGGAGAACCTGAAGGACATCATGCTG
361 F V F H A V K D T I L Q E N L K D I M L

25 ClaI
1141 CAGATCGAT
381 Q

30

35

SEQ ID NO.: 205

40 Human β 2AR-ToxR (5-141) chimera stop GS1 α -ToxR (5-141) chimera transcriptional fusion

SalI +1 B2AR
1 GTCGACATGG GGCAACCCGG GAACGGCAGC GCCTTCTTGC TGGCACCCAA
TGGAAGCCAT

45 61 GCGCCGGACC ACGACGTCAC GCAGCAAAGG GACGAGGTGT GGGTGGTGGG
CATGGGCATC

121 GTCATGTCTC TCATCGTCCT GGCCATCGTG TTTGGCAATG TGCTGGTCAT
50 CACAGCCATT

181 GCCAAGTTCTG AGCGTCTGCA GACGGTCACC AACTACTTCA TCACTTCACT
GGCCTGTGCT

241 GATCTGGTCA TGGGCCTAGC AGTGGTGCCC TTTGGGGCCG CCCATATTCT
TATGAAAATG

55 301 TGGACTTTTG GCAACTTCTG GTGCGAGTTT TGGACTTCCA TTGATGTGCT
GTGCGTCACG

361 GCCAGCATTG AGACCCTGTG CGTGATCGCA GTGGATCGCT ACTTTGCCAT
TACTTCACCT

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421 TTCAAGTACC AGAGCCTGCT GACCAAGAAT AAGGCCCGGG TGATCATTCT
GATGGTGTGG
481 ATTGTGTCTAG GCCTTAYCTC CTTCTTGCCC ATTCAGATGC ACTGGTACAG
GGCCACCCAC
5 541 CAGGAAGCCA TCAACTGCTA TGCCAATGAG ACCTGCTGTG ACTTCTTCAC
GAACCAAGCC
601 TATGCCATTG CCTCTTCCAT CGTGTCTTC TACGTTCCCC TGGTGATCAT
GGTCTTCGTC
661 TACTCCAGGG TCTTTCAGGA GGCCAAAAGG CAGCTCCAGA AGATTGACAA
10 ATCTGAGGGC
721 CGCTTCCATG TCCAGAACCT TAGCCAGGTG GAGCAGGATG GGCGGACGGG
GCATGGACTC
781 CGCAGATCTT CCAAGTTCTG CTTGAAGGAG CACAAAGCCC TCAAGACGTT
AGGCATCATC
15 841 ATGGGCACTT TCACCCTCTG CTGGCTGCCC TTCTTCATCG TTAACATTGT
GCATGTGATC
901 CAGGATAACC TCATCCGTAA GGAAGTTTAC ATCCTCCTAA ATTGGATAGG
CTATGTCAAT
961 TCTGGTTTCA ATCCCCTTAT CTACTGCCGG AGCCCAGATT TCAGGATTGC
20 CTTCCAGGAG
1021 CTTCTGTGCC TGCAGGTC TTCTTTGAAG GCCTATGGCA ATGGCTACTC
CAGCAACGGC
1081 AACACAGGGG AGCAGAGTGG ATATCACGTG GAACAGGAGA AAGAAAATAA
ACTGCTGTGT
25 1141 GAAGACCTCC CAGGCACGGA AGACTTTGTG GGCCATCAAG GTACTGTGCC
TAGCGATAAC

last B2AR linker

sequence
30 1201 ATTGATTCAC AAGGGAGGAA TTGTAGTACA AATGACTCAC TGCTAGAGCG
TGGCCAGACG

PstI +5 toxR (5-141)
1261 GTCACCAACC TGCAGGGACA CAACTCAAAA GAGATATCGA TGAGTCATAT
35 TGGTACTAAA

1321 TTCATTCTTG CTGAAAAATT TACCTTCGAT CCCCTAAGCA ATACTCTGAT
TGACAAAGAA
40 1381 GATAGTGAAG AGATCATTCG ATTAGGCAGC AACGAAAGCC GAATTCTTTG
GCTGCTGGCC
1441 CAACGTCCAA ACGAGGTAAT TTCTCGCAAT GATTTGCATG ACTTTGTTTG
GCGAGAGCAA
1501 GGTTTTGAAG TCGATGATTC CAGCTTAACC CAAGCCATT TCGACTCTGCG
45 CAAAATGCTC
1561 AAAGATTCTGA CAAAGTCCCC ACAATACGTC AAAACGGTTC CGAAGCGCGG
TTACCAATTG
1621 ATCGCCCGAG TGGAAACGGT TGAAGAAGAG ATGGCTCGCG AAAACGAAGC
TGCTCATGAC
50

stop SD XhoI +1 GS1 alpha
1681 ATCTCTTAAT AATCAAGGAG GCCCTCGAGA TGGGCTGCCT CGGGAACAGT
AAGACCGAGG

55 1741 ACCAGCGCAA CGAGGAGAAG GCGCAGCGTG AGGCCAACAA AAAGATCGAG
AAGCAGCTGC
1801 AGAAGGACAA GCAGGTCTAC CGGGCCACGC ACCGCCTGCT GCTGCTGGGT
GCTGGAGAAT

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1861 CTGGTAAAAG CACCATTGTG AAGCAGATGA GGATCCTGCA TGTTAATGGG
TTTAATGGAG
1921 ACAGTGAGAA GGCAACCAAA GTGCAGGACA TCAAAAACAA CCTGAAAGAG
GCCATTGAAA
5 1981 CCATTGTGGC CGCCATGAGC AACCTGGTGC CCCCCGTGGA GCTGGCCAAC
CCCGAGAACC
2041 AGTTCAGAGT GGA CTACATC CTGAGTGTGA TGAACGTGCC TGACTTTGAC
TTCCCTCCCG
2101 AATTCTATGA GCATGCCAAG GCTCTGTGGG AGGATGAAGG AGTGCGTGCC
10 TGCTACGAAC
2161 GCTCCAACGA GTACCAGCTG ATTGACTGTG CCCAGTACTT CCTGGACAAG
ATCGACGTGA
2221 TCAAGCAGGC TGACTATGTG CCGAGCGATC AGGACCTGCT TCGCTGCCGT
GTCCTGACTT
15 2281 CTGGAATCTT TGAGACCAAG TTCCAGGTGG ACAAAGTCAA CTTCCACATG
TTTGACGTGG
2341 GTGGCCAGCG CGATGAACGC CGCAAGTGGA TCCAGTGCTT CAACGATGTG
ACTGCCATCA
2401 TCTTCGTGGT GGCCAGCAGC AGCTACAACA TGGTCATCCG GGAGGACAAC
20 CAGACCAACC
2461 GCCTGCAGGA GGCTCTGAAC CTCTTCAAGA GCATCTGGAA CAACAGATGG
CTGCGCACCA
2521 TCTCTGTGAT CCTGTTCTC AACAAAGCAAG ATCTGCTCGC TGAGAAAGTC
CTTGCTGGGA
25 2581 AATCGAAGAT TGAGGACTAC TTTCCAGAAT TTGCTCGCTA CACTACTCCT
GAGGATGCTA
2641 CTCCCAGGCC CGGAGAGGAC CCACGCGTGA CCCGGGCCAA GTACTTCATT
CGAGATGAGT
2701 TTCTGAGGAT CAGCACTGCC AGTGGAGATG GCGGTCCTA CTGCTACCCCT
30 CATTTACCT
2761 GCGCTGTGGA CACTGAGAAC ATCCGCCGTG TGTTCACGA CTGCCGTGAC
ATCATTGAGC

ClaI +5 toxR (5-141)

35 2821 GCATGCACCT TCGTCAGTAC GAGCTGCTCA TCGATGGACA CAACTCAAAA
GAGATATCGA

2881 TGAGTCATAT TGGTACTAAA TTCATTCTTG CTGAAAAATT TACCTTCGAT
40 CCCCTAAGCA
2941 ATACTCTGAT TGACAAAGAA GATAGTGAAG AGATCATTCG ATTAGGCAGC
AACGAAAGCC
3001 GAATTCTTTG GCTGCTGGCC CAACGTCCAA ACGAGGTAAT TTCTCGCAAT
GATTTCATG
45 3061 ACTTTGTTTG GCGAGAGCAA GGTTTTGAAG TCGATGATTC CAGCTTAACC
CAAGCCATTT
3121 CGACTCTGCG CAAAATGCTC AAAGATTGGA CAAAGTCCCC ACAATACGTC
AAAACGGTTC
3181 CGAAGCGCGG TTACCAATTG ATCGCCCGAG TGGAAACGGT TGAAGAAGAG
50 ATGGCTCGCG

Stop XbaI Stem-

loop
3241 AAAACGAAGC TGCTCATGAC ATCTCTTAAT AATCTAGAGG ATCCCCGCGC
55 CCTCATCCGA
3301 AAGGGCG

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SEQ ID NO.: 208

Vibrio cholerae Pctx::lacZ reporter fusion construct

5

XbaI
1 TCTAGAGGCT GTGGGTAGAA GTGAAACGGG GTTTACCGAT AAAAAACAGAA
AATGATAAAA

10

3 ToxR binding repeats
61 AAGGACTAAA TAGTATATTT TGATTTTGA TTTTGGATT CAAATAATAC
AAATTTATTT

+1

15

lacZ
121 ACTTATTTTAA TTGTTTGGAT CAATTATTTT TCTGTTAAAC AAAGGGAGCA
TTATATGGTA

20

181 AAGACCATGA TTACGGATTC ACTGGCCGTC GTTTTACAAC GTCGTGACTG
GGAAAACCCCT
241 GCGGTTACCC AACTTAATCG CCTTGCAGCA CATCCCCCTT TCGCCAGCTG
GCGTAATAGC

25

301 GAAGAGGCCC GCACCGATCG CCCTTCCCAA CAGTTGCGCA GCCTGAATGG
CGAATGGCGC
361 TTTCCTGGT TTCCGGCACC AGAAGCGGTG CCGGAAAGCT GGCTGGAGTG
CGATCTTCCT

30

421 GAGGCCGATA CTGTCGTCGT CCCCTCAAAC TGGCAGATGC ACGGTTACGA
TGCGCCCATC
481 TACACCAACG TGACCTATCC CATTACGGTC AATCCGCCGT TTGTTCCAC
GGAGAATCCG

35

541 ACGGGTTGTT ACTCGCTCAC ATTTAATGTT GATGAAAGCT GGCTACAGGA
AGGCCAGACG
601 CGAATTATTT TTGATGGCGT TAACTCGGCG TTTCATCTGT GGTGCAACGG
GCGCTGGGTC

40

661 GGTACGGCC AGGACAGTCG TTTGCCGTCT GAATTGACC TGAGCGCAT
TTTACGCGCC
721 GGAGAAAACC GCCTCGCGGT GATGGTGCTG CGCTGGAGTG ACGGCAGTTA
TCTGGAAGAT

45

781 CAGGATATGT GCGGGATGAG CGGCATTTTC CGTGACGTCT CGTTGCTGCA
TAAACCGACT
841 ACACAAATCA GCGATTTCCA TGTTGCCACT CGCTTTAATG ATGATTTTCA
CCGCGCTGTA

50

901 CTGGAGGCTG AAGTTCAGAT GTGCGGCGAG TTGCGTGACT ACCTACGGGT
AACAGTTTCT
961 TTATGGCAGG GTGAAACGCA GGTGCGCCAGC GGCACCGCGC CTTTCGGCGG
TGAAATTATC

55

1021 GATGAGCGTG GTGGTTATGC CGATCGCGTC AACTACGTC TGAACGTCGA
AAACCCGAAA
1081 CTGTGGAGCG CCGAAATCCC GAATCTCTAT CGTGCGGTGG TTGAACTGCA
CACCGCCGAC

1141 GGCACGCTGA TTGAAGCAGA AGCCTGCGAT GTCGGTTTCC GCGAGGTGCG
GATTGAAAAT
1201 GGTCTGCTGC TGCTGAACGG CAAGCCGTTG CTGATTCGAG GCGTTAACCG
TCACGAGCAT

1261 CATCCTCTGC ATGGTCAGGT CATGGATGAG CAGACGATGG TGCAGGATAT
CCTGCTGATG
1321 AAGCAGAACA ACTTTAACGC CGTGCGCTGT TCGCATTATC CGAACCATCC
GCTGTGGTAC

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1381 ACGCTGTGCG ACCGCTACGG CCTGTATGTG GTGGATGAAG CCAATATTGA
AACCCACGGC
1441 ATGGTGCCAA TGAATCGTCT GACCGATGAT CCGCGCTGGC TACCGGCGAT
GAGCGAACGC
5 1501 GTAACGCGAA TGGTGACGCG CGATCGTAAT CACCCGAGTG TGATCATCTG
GTCGCTGGGG
1561 AATGAATCAG GCCACGGCGC TAATCACGAC GCGCTGTATC GCTGGATCAA
ATCTGTCTGAT
1621 CCTTCCCGCC CGGTGCAGTA TGAAGGCGGC GGAGCCGACA CCACGGCCAC
10 CGATATTATT
1681 TGCCCGATGT ACGCGCGCGT GGATGAAGAC CAGCCCTTCC CGGCTGTGCC
GAAATGGTCC
1741 ATCAAAAAT GGCTTTCGCT ACCTGGAGAG ACGCGCCCGC TGATCCTTTG
CGAATACGCC
1801 CACGCGATGG GTAACAGTCT TGGCGTTTC GCTAAATACT GGCAGGCGTT
TCGTCAGTAT
1861 CCCCCTTTAC AGGGCGGCTT CGTCTGGGAC TGGGTGGATC AGTCGCTGAT
TAAATATGAT
1921 GAAAACGGCA ACCCGTGGTC GGCTTACGGC GGTGATTTTG GCGATACGCC
20 GAACGATCGC
1981 CAGTTCTGTA TGAACGGTCT GGTCTTTGCC GACCGCACGC CGCATCCAGC
GCTGACGGAA
2041 GCAAAACACC AGCAGCAGTT TTTCCAGTTC CGTTTATCCG GGCAAACCAT
CGAAGTGACC
2101 AGCGAATACC TGTTCGTC TAGCGATAAC GAGCTCCTGC ACTGGATGGT
25 GGCGCTGGAT
2161 GGTAAGCCGC TGGCAAGCGG TGAAGTGCCT CTGGATGTCG CTCCACAAGG
TAAACAGTTG
2221 ATTGAAGTGC CTGAACTACC GCAGCCGGAG AGCGCCGGGC AACTCTGGCT
30 CACAGTACGC
2281 GTAGTGCAAC CGAACGCGAC CGCATGGTCA GAAGCCGGGC ACATCAGCGC
CTGGCAGCAG
2341 TGGCGTCTGG CGGAAAACCT CAGTGTGACG CTCCCCGCCG CGTCCCACGC
CATCCCGCAT
2401 CTGACCACCA GCGAAATGGA TTTTTCATC GAGCTGGGTA ATAAGCGTTG
35 GCAATTTAAC
2461 CGCCAGTCAG GCTTTCTTTC ACAGATGTGG ATTGGCGATA AAAAAACACT
GCTGACGCCG
2521 CTGCGCGATC AGTTCACCCG TGCACCGCTG GATAACGACA TTGGCGTAAG
40 TGAAGCGACC
2581 CGCATTGACC CTAACGCCTG GGTGGAACGC TGGAAAGCGG CGGGCCATTA
CCAGGCCGAA
2641 GCAGCGTTGT TGCAGTGAC GGCAGATACA CTTGCTGATG CGGTGCTGAT
TACGACCGCT
2701 CACGCGTGGC AGCATCAGGG GAAAACCTTA TTTATCAGCC GGAAAACCTA
45 CCGGATTGAT
2761 GGTAGTGGTC AAATGGCGAT TACCGTTGAT GTTGAAGTGG CGAGCGATAC
ACCGCATCCG
2821 GCGCGGATTG GCCTGAACTG CCAGCTGGCG CAGGTAGCAG AGCGGGTAAA
50 CTGGCTCGGA
2881 TTAGGGCCGC AAGAAAATA TCCCGACCGC CTTACTGCCG CCTGTTTTGA
CCGCTGGGAT
2941 CTGCCATTGT CAGACATGTA TACCCCGTAC GTCTTCCCGA GCGAAAACGG
TCTGCGCTGC
3001 GGGACGCGC AATTGAATTA TGGCCACAC CAGTGGCGCG GCGACTTCCA
55 GTTCAACATC
3061 AGCCGCTACA GTCAACAGCA ACTGATGGAA ACCAGCCATC GCCATCTGCT
GCACGCGGAA
3121 GAAGGCACAT GGCTGAATAT CGACGGTTTC CATATGGGGA TTGGTGGCGA
60 CGACTCCTGG

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3181 AGCCCGTCAG TATCGGCGGA ATTCCAGCTG AGCGCCGGTC GCTACCATTA
CCAGTTGGTC

5 3241 TGGTGTCAAA AATAATAACGCCCTCAT CCGAAAGGGC GTCTAGA
Stop Stem-loop XbaI

SEQ ID NO.: 266

10 pMPX-74 MalE (1-28) fusion vector

2401 GAATTCAGGCGCTTTTTTAGACTGGTCGTAATGAAATTCAGGAGGTTCTGCATATGAAAAT
1 M K I
15 2461 AAAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTC
4 K T G A R I L A L S A L T T M M F S A S
20 2521 GGCTCTCGCCAAAATCATCGAAGCCCGCCTGCAGGCCTCGGTTCGACGCCGAATCTAGAGA
24 A L A K I I E A R L Q A S V D A E S R D
25 2581 TTATAAAGATGACGATGACAAATAATAAGCTAGAGG (transcriptional stop)
44 Y K D D D D K
FLAG lost XbaI

pMPX-72::male(1-28)::FXa::PstI, SalI, XbaI::FLAG
Rhamnose inducible, clone into PstI, SalI, XbaI

30 Made by cutting TOPO NsiI-male (1-28)::FXa::PstI, SalI, XbaI::FLAG-
NheI insertion with NsiI & NheI and cloning into pMPX-72 cut with PstI
& XbaI.

SEQ ID NO.: 267

40 pMPX-75 Male (1-28) fusion vector

1621 CCATACCCGTTTTTTTTGGGCTAGCAGGAGGCCCTGCATATGAAAATAAAAAACAGGTGCAC
1 M K I K T G A
45 1681 GCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTCGGCTCTCGCCAAAA
8 R I L A L S A L T T M M F S A S A L A K
50 1741 TCATCGAAGCCCGCCTGCAGGCCTCGGTTCGACGCCGAATCTAGAGATTATAAAGATGACG
Factor Xa PstI SalI XbaI FLAG
1801 ATGACAAATAATAAGCTAGAGG (Transcriptional stop)
Lost XbaI

55 pMPX-71::male(1-28)::FXa::PstI, SalI, XbaI::FLAG
Arabinose inducible, clone into PstI, SalI, XbaI

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Made by cutting TOPO NsiI-male (1-28)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & NheI and cloning into pMPX-71 cut with PstI & XbaI.

5

SEQ ID NO.: 268

pMPX-88 Male (1-28) fusion vector

10

```

                                     SD old PstI +1
                                     AGGAGGTTCTGCATATGAAAAT
1                                     M K I
15
      AAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTC
4      K T G A R I L A L S A L T T M M F S A S
      Factor Xa PstI SalI XbaI
20      GGCTCTCGCCAAAATCATCGAAGCCCGCCTGCAGGCCTCGGTCGACGCCGAATCTAGAGA
24      A L A K I I E A R L Q A S V D A E S R D
      FLAG lost XbaI
25      TTATAAAGATGACGATGACAAATAATAAGCTAGAGGTACC (transcriptional
stop)
44      Y K D D D D K
```

30 pMPX-84::male(1-28)::FXa::PstI, SalI, XbaI::FLAG
Temperature inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-male (1-28)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & NheI and cloning into pMPX-84 cut with PstI & XbaI.

35

SEQ ID NO.: 269

40

pMPX-93 Male (1-28) fusion vector

```

                                     SD old PstI +1
                                     AGGAGGTTCTGCATATGAAAAT
45                                     M K I
      AAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTC
4      K T G A R I L A L S A L T T M M F S A S
      Factor Xa PstI SalI XbaI
50      GGCTCTCGCCAAAATCATCGAAGCCCGCCTGCAGGCCTCGGTCGACGCCGAATCTAGAGA
24      A L A K I I E A R L Q A S V D A E S R D
      FLAG lost XbaI
55      TTATAAAGATGACGATGACAAATAATAAGCTAGAGGTACC (transcriptional
stop)
44      Y K D D D D K
```

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pMPX-86::male(1-28)::FXa::PstI, SalI, XbaI::FLAG
Temperature inducible, clone into PstI, SalI, XbaI

- 5 Made by cutting TOPO NsiI-male (1-28)::FXa::PstI, SalI, XbaI::FLAG-
NheI insertion with NsiI & NheI and cloning into pMPX-86 cut with PstI & XbaI.

SEQ ID NO.: 270

- 10 pMPX-77 Male (1-370 del 354-364) fusion vector

			SD old PstI +1
2401	GAATTCAGGCGCTTTTTAGACTGGTCGTAATGAAATTCAGGAGGTTCTGCATATGAAAAAT		M K I
1			
15	2461	AAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTTCCGCCTC	
4		K T G A R I L A L S A L T T M M F S A S	
2521	GGCTCTCGCCAAAATCGAAGAAGGTAAACTGGTAATCTGGATTAAACGGCGATAAAGGCTA		
20	24	A L A K I E E G K L V I W I N G D K G Y	
2581	TAACGGTCTCGCTGAAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAAGTCACCGT		
44		N G L A E V G K K F E K D T G I K V T V	
25	2641	TGAGCATCCGATAAACTGGAAGAGAAATTCACAGGTTGCGGCAACTGGCGATGGCCC	
64		E H P D K L E E K F P Q V A A T G D G P	
2701	TGACATTATCTTCTGGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGC		
84		D I I F W A H D R F G G Y A Q S G L L A	
30	2761	TGAAATCACCCCGGACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGGGATGCCGT	
104		E I T P D K A F Q D K L Y P F T W D A V	
2821	ACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGATTTA		
35	124	R Y N G K L I A Y P I A V E A L S L I Y	
2881	TAACAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGCGCTGGATAA		
144		N K D L L P N P P K T W E E I P A L D K	
40	2941	AGAACTGAAAGCGAAAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTACTTCAC	
164		E L K A K G K S A L M F N L Q E P Y F T	
3001	CTGGCCGCTGATTGCTGCTGACGGGGGTTATGCGTTCAAGTATGAAAACGGCAAGTACGA		
184		W P L I A A D G G Y A F K Y E N G K Y D	
45	3061	CATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCGGTCTGACCTTCTGGTTGA	
204		I K D V G V D N A G A K A G L T F L V D	
3121	CCTGATTAAAAACAAACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCTGCCTT		
50	224	L I K N K H M N A D T D Y S I A E A A F	
3181	TAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATCGACAC		
244		N K G E T A M T I N G P W A W S N I D T	
55	3241	CAGCAAAGTGAATTATGGTGTAAACGGTACTGCCGACCTTCAAGGGTCAACCATCCAAACC	
264		S K V N Y G V T V L P T F K G Q P S K P	
3301	GTTCGTTGGCGTGCTGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGCTGGCGAA		

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284 F V G V L S A G I N A A S P N K E L A K

3361 AGAGTTCTCTCGAAAACATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAAGACAA
304 E F L E N Y L L T D E G L E A V N K D K

5 3421 ACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCACGTAT
324 P L G A V A L K S Y E E E L A K D P R I

10 pMPX-72::malE(1-370 del 354-364)::FXa::PstI, SalI, XbaI::FLAG
Rhamnose inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-malE (1-370 del 354-364)::FXa::PstI, SalI,
XbaI::FLAG-NheI insertion with NsiI & NheI and cloning into pMPX-72
cut with PstI & XbaI.

15

SEQ ID NO.: 271

20 pMPX-76 MalE (1-370 del 354-364) fusion vector

1621 CCATACCCGTTTTTTTTGGGCTAGCAGGAGGCCCTGCATATGAAAATAAAACAGGTGCAC
1 M K I K T G A

25 1681 GCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTCGGCTCTCGCCAAAA
8 R I L A L S A L T T M M F S A S A L A K

1741 TCGAAGAAGGTAAACTGGTAATCTGGATTAACGGCGATAAAGGCTATAACGGTCTCGCTG
28 I E E G K L V I W I N G D K G Y N G L A

30 1801 AAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAAGTCACCGTTGAGCATCCGGATA
48 E V G K K F E K D T G I K V T V E H P D

35 1861 AACTGGAAGAGAAATTCCCACAGGTTGCGGCAACTGGCGATGGCCCTGACATTATCTTCT
68 K L E E K F P Q V A A T G D G P D I I F

1921 GGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGCTGAAATCACCCCGG
88 W A H D R F G G Y A Q S G L L A E I T P

40 1981 ACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGGGATGCCGTACGTTACAACGGCA
108 D K A F Q D K L Y P F T W D A V R Y N G

2041 AGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGATTTATAACAAAGATCTGC
128 K L I A Y P I A V E A L S L I Y N K D L

45 2101 TGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCGCTGGATAAAGAACTGAAAGCGA
148 L P N P P K T W E E I P A L D K E L K A

2161 AAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTACTTCACCTGGCCGCTGATTG
50 168 K G K S A L M F N L Q E P Y F T W P L I

2221 CTGCTGACGGGGTTATGCGTTCAAGTATGAAAACGGCAAGTACGACATTAAAGACGTGG
188 A A D G G Y A F K Y E N G K Y D I K D V

55 2281 GCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCCTGGTTGACCTGATTAAAAACA
208 G V D N A G A K A G L T F L V D L I K N

2341 AACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAA
228 K H M N A D T D Y S I A E A A F N K G E

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2401 CAGCGATGACCATCAACGGCCCCGTGGGCATGGTCCAACATCGACACCAGCAAAGTGAATT
248 T A M T I N G P W A W S N I D T S K V N

5 2461 ATGGTGTAACGGTACTGCCGACCTTCAAGGGTCAACCATCCAAACCGTTCGTTGGCGTGC
268 Y G V T V L P T F K G Q P S K P F V G V

2521 TGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGCTGGCGAAAGAGTTCCTCGAAA
288 L S A G I N A A S P N K E L A K E F L E

10 2581 ACTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAAGACAAACCGCTGGGTGCCG
308 N Y L L T D E G L E A V N K D K P L G A

2641 TAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCACGTATTGCCGCCACCATGG
15 328 V A L K S Y E E E L A K D P R I A A T M

2701 Factor Xa PstI
348 AAAACGCCCAGTCCGCTTTCTGGTATGCCGTGCGTATCGAAGCCCGCTGCAGGCCTCGG
20 E N A Q S A F W Y A V R I E A R L Q A S

2761 Sali XbaI FLAG Lost XbaI
TCGACGCCGAATCTAGAGATTATAAAGATGACGATGACAAATAATAAGCTAGAGGA (trxn stop)
368 V D A E S R D Y K D D D D K

25 pMPX-71::malE(1-370 del 354-364)::FXa::PstI, Sali, XbaI::FLAG
Arabinose inducible, clone into PstI, Sali, XbaI

30 Made by cutting TOPO NsiI-malE (1-370 del 354-364)::FXa::PstI, Sali,
XbaI::FLAG-NheI insertion with NsiI & NheI and cloning into pMPX-71 cut with PstI &
XbaI.

35 SEQ ID NO.: 272

pMPX-89 MalE (1-370 del 354-364) fusion vector

40 SD old PstI +1
AGGAGGTTCTGCATATGAAAAATAAAACAGGTGCAC
1 M K I K T G A

8 GCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTCGGCTCTCGCCAAAA
R I L A L S A L T T M M F S A S A L A K

45 28 TCGAAGAAGGTAAACTGGTAATCTGGATTAACGGCGATAAAGGCTATAACGGTCTCGCTG
I E E G K L V I W I N G D K G Y N G L A

50 48 AAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAGTCACCGTTGAGCATCCGGATA
E V G K K F E K D T G I K V T V E H P D

68 AACTGGAAGAGAAATTCACACAGGTTGCGGCAACTGGCGATGGCCCTGACATTATCTTCT
K L E E K F P Q V A A T G D G P D I I F

55 88 GGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGCTGAAATCACCCCGG
W A H D R F G G Y A Q S G L L A E I T P

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108 ACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGGGATGCCGTACGTTACAACGGCA
D K A F Q D K L Y P F T W D A V R Y N G

5 128 AGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGATTTATAACAAAGATCTGC
K L I A Y P I A V E A L S L I Y N K D L

148 TGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCGCTGGATAAAGAACTGAAAGCGA
L P N P P K T W E E I P A L D K E L K A

10 168 AAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTACTTCACCTGGCCGCTGATTG
K G K S A L M F N L Q E P Y F T W P L I

15 188 CTGCTGACGGGGGTTATGCGTTCAAGTATGAAAACGGCAAGTACGACATTAAAGACGTGG
A A D G G Y A F K Y E N G K Y D I K D V

208 GCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCCTGGTTGACCTGATTAAAAACA
G V D N A G A K A G L T F L V D L I K N

20 228 AACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAA
K H M N A D T D Y S I A E A A F N K G E

248 CAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATCGACACCAGCAAAGTGAATT
T A M T I N G P W A W S N I D T S K V N

25 268 ATGGTGTAAACGGTACTGCCGACCTTCAAGGGTCAACCATCCAAACCGTTCGTTGGCGTGC
Y G V T V L P T F K G Q P S K P F V G V

288 TGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGCTGGCGAAAGAGTTCTCTCGAAA
L S A G I N A A S P N K E L A K E F L E

30 308 ACTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAAGACAAACCGCTGGGTGCCG
N Y L L T D E G L E A V N K D K P L G A

35 328 TAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCACGTATTGCCGCCACCATGG
V A L K S Y E E E L A K D P R I A A T M

Factor Xa PstI
40 348 AAAACGCCCAGTCCGCTTTCTGGTATGCCGTGCGTATCGAAGCCCCGCTGCAGGCCTCGG
E N A Q S A F W Y A V R I E A R L Q A S

Sali XbaI FLAG Lost XbaI
TCGACGCCGAATCTAGAGATTATAAAGATGACGATGACAAATAATAAGCTAGAGG
(trxn stop)
368 V D A E S R D Y K D D D D K

45 pMPX-84::male(1-370 del 354-364)::FXa::PstI, Sali, XbaI::FLAG
Temperature inducible, clone into PstI, Sali, XbaI

50 Made by cutting TOPO NsiI-male (1-370 del 354-364)::FXa::PstI, Sali,
XbaI::FLAG-NheI insertion with NsiI & NheI and cloning into pMPX-84
cut with PstI & XbaI.

SEQ ID NO.: 273

55 pMPX-94 Male (1-370 del 354-364) fusion vector

SD old PstI +1
AGGAGGTTCTGCATATGAAAATAAAAACAGGTGCAC

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1 M K I K T G A

8 GCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTCGGCTCTCGCCAAAA
R I L A L S A L T T M M F S A S A L A K

5 28 TCGAAGAAGGTAAACTGGTAATCTGGATTAACGGCGATAAAGGCTATAACGGTCTCGCTG
I E E G K L V I W I N G D K G Y N G L A

10 48 AAGTCGGTAAGAAATTCGAGAAAGATAACCGGAATTAAAGTCACCGTTGAGCATCCGGATA
E V G K K F E K D T G I K V T V E H P D

68 AACTGGAAGAGAAATTCACACAGGTTGCGGCAACTGGCGATGGCCCTGACATTATCTTCT
K L E E K F P Q V A A T G D G P D I I F

15 88 GGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGCTGAAATCACCCCGG
W A H D R F G G Y A Q S G L L A E I T P

108 ACAAAGCGTTCAGGACAAGCTGTATCCGTTTACCTGGGATGCCGTACGTTACAACGGCA
D K A F Q D K L Y P F T W D A V R Y N G

20 128 AGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGATTTATAACAAAGATCTGC
K L I A Y P I A V E A L S L I Y N K D L

148 TGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCGCTGGATAAAGAACTGAAAGCGA
L P N P P K T W E E I P A L D K E L K A

25 168 AAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTACTTCACCTGGCCGCTGATTG
K G K S A L M F N L Q E P Y F T W P L I

30 188 CTGCTGACGGGGGTTATGCGTTCAAGTATGAAAACGGCAAGTACGACATTAAAGACGTGG
A A D G G Y A F K Y E N G K Y D I K D V

208 GCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCCTGGTTGACCTGATTAAAAACA
G V D N A G A K A G L T F L V D L I K N

35 228 AACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAA
K H M N A D T D Y S I A E A A F N K G E

40 248 CAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATCGACACCAGCAAAGTGAATT
T A M T I N G P W A W S N I D T S K V N

268 ATGGTGTAACGGTACTGCCGACCTTCAAGGGTCAACCATCCAAACCGTTCTGTTGGCGTGC
Y G V T V L P T F K G Q P S K P F V G V

45 288 TGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGCTGGCGAAAGAGTTCTCTGAAA
L S A G I N A A S P N K E L A K E F L E

308 ACTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAAGACAAACCGCTGGGTGCCG
N Y L L T D E G L E A V N K D K P L G A

50 328 TAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCACGTATTGCCGCCACCATGG
V A L K S Y E E E L A K D P R I A A T M

55 348 AAAACGCCCAGTCCGCTTTCTGGTATGCCGTGCGTATCGAAGCCCGCTGCGAGGCCTCGG
E N A Q S A F W Y A V R I E A R L Q A S

60 (trxn stop)

Factor Xa PstI

Sali XbaI FLAG Lost XbaI

TCGACGCCGAATCTAGAGATTATAAAGATGACGATGACAAATAATAAGCTAGAGG

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368 V D A E S R D Y K D D D D K

5 pMPX-86::male(1-370 del 354-364)::FXa::PstI, SalI, XbaI::FLAG
Temperature inducible, clone into PstI, SalI, XbaI

10 Made by cutting TOPO NsiI-male (1-370 del 354-364)::FXa::PstI, SalI,
XbaI::FLAG-NheI insertion with NsiI & NheI and cloning into pMPX-86
cut with PstI & XbaI.

SEQ ID NO.: 274

15 pMPX-79 TrxA (2-109 del 103-107) fusion vector

103-107) SD PstI SalI XbaI +2 trxA(del
1 TAGCAGGAGGCCCTGCAGGCCTCGGTCGACGCCGAATCTAGAAAGCGATAAAATTATT
1 A S V D A E S R S D K I I
20 61 CACCTGACTGACGACAGTTTTGACACGGATGTACTCAAAGCGGACGGGGCGATCCTCGTC
17 H L T D D S F D T D V L K A D G A I L V
121 GATTTCTGGGCAGAGTGGTGCGGTCCGTGCAAAATGATCGCCCCGATTCTGGATGAAATC
25 37 D F W A E W C G P C K M I A P I L D E I
181 GCTGACGAATATCAGGGCAAACCTGACCGTTGCAAACTGAACATCGATCAAAACCTGGC
57 A D E Y Q G K L T V A K L N I D Q N P G
30 241 ACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTGCTGTTCAAAACGGTGAA
77 T A P K Y G I R G I P T L L L F K N G E
301 GTGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTGAAAGAGAACCTGGCGGAT
97 V A A T K V G A L S K G Q L K E N L A D
35
FLAG Lost XbaI
361 TATAAAGATGACGATGACAAATAATAAGCTAGAGG (transcriptional stop)
40 117 Y K D D D D K

pMPX-71::PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG
Arabinose inducible, clone into PstI, SalI, XbaI
+1 Met required for protein to be fused

45 Made by cutting TOPO PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG-
NheI insertion with PstI & NheI and cloning into pMPX-71 cut with PstI & XbaI.

50 SEQ ID NO.: 275

pMPX-78 TrxA (2-109 del 103-107) fusion vector

55 1 GAATTCAGGCGCTTTTTAGACTGGTCGTAATGAAATTCAGGAGGTTCTGCAGGCCTC
1 A S

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SalI XbaI +2 trxA(del 103-107)

61 GGTCGACGCCGAATCTAGAAGCGATAAAATTATTCACCTGACTGACGACAGTTTTTGACAC
6 V D A E S R S D K I I H L T D D S F D T

5 121 GGATGTACTCAAAGCGGACGGGGCGATCCTCGTCTGATTTCTGGGCAGAGTGGTGCGGTCC
26 D V L K A D G A I L V D F W A E W C G P

181 GTGCAAAATGATCGCCCCGATTCTGGATGAAATCGCTGACGAATATCAGGGCAAACCTGAC
46 C K M I A P I L D E I A D E Y Q G K L T

10 241 CGTTGCAAACTGAACATCGATCAAAACCTGGCACTGCGCCGAAATATGGCATCCGTGG
66 V A K L N I D Q N P G T A P K Y G I R G

301 TATCCCGACTCTGCTGCTGTTCAAAAACGGTGAAGTGGCGGCAACCAAAGTGGGTGCACT
15 86 I P T L L L F K N G E V A A T K V G A L

FLAG

361
GTCTAAAGGTCAGTTGAAAGAGAACCTGGCGGATTATAAAGATGACGATGACAAATAATAA
20 106 S K G Q L K E N L A D Y K D D D D K

lost XbaI
GCTAGAGG (transcriptional stop)

25 pMPX-72::PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG
Rhamnose inducible, clone into PstI, SalI, XbaI
+1 Met required for protein to be fused

Made by cutting TOPO PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG-
30 NheI insertion with PstI & NheI and cloning into pMPX-72 cut with PstI
& XbaI.

35 SEQ ID NO.: 276

pMPX-90 TrxA (2-109 del 103-107) fusion vector

SD PstI SalI XbaI +2 trxA(del

40 103-107)
AGGAGGTTCTGCAGGCCTCGGTGACGCCGAATCTAGAAGCGATAAAATTATT
1 A S V D A E S R S D K I I

CACCTGACTGACGACAGTTTTGACACGGATGTACTCAAAGCGGACGGGGCGATCCTCGTC
45 17 H L T D D S F D T D V L K A D G A I L V

GATTTCTGGGCAGAGTGGTGCGGTCCGTGCAAAATGATCGCCCCGATTCTGGATGAAATC
37 D F W A E W C G P C K M I A P I L D E I

50 GCTGACGAATATCAGGGCAAACCTGACCGTTGCAAACTGAACATCGATCAAAACCTGGC
57 A D E Y Q G K L T V A K L N I D Q N P G

ACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTGCTGTTCAAAAACGGTGAA
77 T A P K Y G I R G I P T L L L F K N G E

55 GTGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTGAAAGAGAACCTGGCGGAT
97 V A A T K V G A L S K G Q L K E N L A D

FLAG Lost XbaI

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TATAAAGATGACGATGACAAATAATAAGCTAGAGGTACC (transcriptional
stop)
117 Y K D D D D K

- 5 pMPX-84::PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG
Temperature inducible, clone into PstI, SalI, XbaI
+1 Met required for protein to be fused

- 10 Made by cutting TOPO PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG-
NheI insertion with PstI & NheI and cloning into pMPX-84 cut with PstI
& XbaI.

SEQ ID NO.: 277

- 15 pMPX-95 TrxA (2-109 del 103-107) fusion vector

SD PstI SalI XbaI +2 trxA(del
103-107)
20 AGGAGGTTCTGCAGGCCTCGGTTCGACGCCGAATCTAGAAGCGATAAAATTATT
1 A S V D A E S R S D K I I
CACCTGACTGACGACAGTTTTGACACGGATGTACTCAAAGCGGACGGGGCGATCCTCGTC
17 H L T D D S F D T D V L K A D G A I L V
25 GATTTCTGGGCAGAGTGGTGCAGTCCGTGCAAAATGATCGCCCCGATTCTGGATGAAATC
37 D F W A E W C G P C K M I A P I L D E I
GCTGACGAATATCAGGGCAAACCTGACCGTTGCAAACTGAACATCGATCAAAACCTGGC
30 57 A D E Y Q G K L T V A K L N I D Q N P G
ACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTGCTGTTCAAAAACGGTGAA
77 T A P K Y G I R G I P T L L L F K N G E
35 GTGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTGAAAGAGAACCTGGCGGAT
97 V A A T K V G A L S K G Q L K E N L A D

FLAG Lost XbaI
40 **TATAAAGATGACGATGACAAATAATAAGCTAGAGGTACC** (transcriptional
stop)
117 Y K D D D D K

- 45 pMPX-86::PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG
Temperature inducible, clone into PstI, SalI, XbaI
+1 Met required for protein to be fused

- 50 Made by cutting TOPO PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG-
NheI insertion with PstI & NheI and cloning into pMPX-86 cut with PstI
& XbaI.

SEQ ID NO.: 278

- 55 pMPX-80 MalE (1-28) MCS TrxA (2-109 del 103-107) fusion vector

SD Lost PstI +1
male(1-28)
2401 GAATTCAGGCGCTTTTTAGACTGGTCGTAATGAAATTCAGGAGGTTCTGCATATGAAAAT

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1 M K I

2461 AAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTC
4 K T G A R I L A L S A L T T M M F S A S

5

2521 GGCTCTCGCCAAAATCATCGAAGCCCGCCTGCAGGCCTCGGTGCAGCGCCGAATCTAGAAG
24 A L A K I I E A R L Q A S V D A E S R S

10 +2 trxA (2-109 del 103-107)
2581 CGATAAAATTATTACCTGACTGACGACAGTTTTTGACACGGATGTACTCAAAGCGGACGG
44 D K I I H L T D D S F D T D V L K A D G

15 2641 GGCGATCCTCGTCGATTTCTGGGCAGAGTGGTGCGGTCCGTGCAAAATGATCGCCCCGAT
64 A I L V D F W A E W C G P C K M I A P I

2701 TCTGGATGAAATCGCTGACGAATATCAGGGCAAACCTGACCGTTGCAAACTGAACATCGA
84 L D E I A D E Y Q G K L T V A K L N I D

20 2761 TCAAAACCCTGGCACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTGCTGTT
104 Q N P G T A P K Y G I R G I P T L L L F

2821 CAAAAACGGTGAAGTGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTGAAAGA
124 K N G E V A A T K V G A L S K G Q L K E

25

2881 GAACCTGGCGGATTATAAAGATGACGATGACAAAATAATAAGCTAGAGG (trxn stop)
144 N L A D Y K D D D D K

30 pMPX-72::malE(1-28)::FXa::PstI, SalI, XbaI::TrxA(1-109 del 103-107)::FLAG
Rhamnose inducible, clone into PstI, SalI, XbaI

35 Made by cutting TOPO NsiI-malE (1-28)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & XbaI and cloning into pMPX-78 cut with PstI & XbaI.

SEQ ID NO.: 279

40 pMPX-81 MalE (1-28) MCS TrxA (2-109 del 103-107) fusion vector

1621 CCATACCCGTTTTTTTTGGGCTAGCAGGAGGCCCTGCATATGAAAATAAAAACAGGTGCAC
1 M K I K T G A

45 1681 GCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTCGGCTCTCGCCAAAA
8 R I L A L S A L T T M M F S A S A L A K

50 del Factor Xa PstI SalI +2 trxA(2-109 XbaI
103-107)
1741 TCATCGAAGCCCGCCTGCAGGCCTCGGTGCAGCGCCGAATCTAGAAGCGATAAAATTATTC
28 I I E A R L Q A S V D A E S R S D K I I

55 1801 ACCTGACTGACGACAGTTTTTGACACGGATGTACTCAAAGCGGACGGGGCGATCCTCGTCG
48 H L T D D S F D T D V L K A D G A I L V

1861 ATTTCTGGGCAGAGTGGTGCGGTCCGTGCAAAATGATCGCCCCGATTCTGGATGAAATCG
68 D F W A E W C G P C K M I A P I L D E I

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1921 CTGACGAATATCAGGGCAAACCTGACCGTTGCAAACTGAACATCGATCAAAACCCTGGCA
88 A D E Y Q G K L T V A K L N I D Q N P G

5 1981 CTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTGCTGTTCAAAAACGGTGAAG
108 T A P K Y G I R G I P T L L L F K N G E

2041 TGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTGAAAGAGAACCTGGCGGATT
128 V A A T K V G A L S K G Q L K E N L A D

10

FLAG
2101 ATAAAGATGACGATGACAAATAATAAGCTAGAGG (transcriptional stop)
148 Y K D D D D K

15 pMPX-71::male(1-28)::FXa::PstI, SalI, XbaI::TrxA(1-109 del 103-
107)::FLAG
Arabinose inducible, clone into PstI, SalI, XbaI

20 Made by cutting TOPO NsiI-male (1-28)::FXa::PstI, SalI, XbaI::FLAG-
NheI insertion with NsiI & XbaI and cloning into pMPX-79 cut with PstI
& XbaI.

SEQ ID NO.: 280

25 pMPX-91 Male (1-28) MCS TrxA (2-109 del 103-107) fusion vector

male(1-28)

SD Lost PstI +1

30 AGGAGGTTCTGCATATGAAAAT
1 M K I

AAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTC
4 K T G A R I L A L S A L T T M M F S A S

35

Factor Xa PstI SalI XbaI
GGCTCTCGCCAAAATCATCGAAGCCCGCTGCAGGCCTCGGTTCGACGCCGAATCTAGAAG
24 A L A K I I E A R L Q A S V D A E S R S

40 +2 trxA (2-109 del 103-107)

CGATAAAATTATTACCTGACTGACGACAGTTTTGACACGGATGTACTCAAAGCGGACGG
44 D K I I H L T D D S F D T D V L K A D G

GGCGATCCTCGTCGATTCTCTGGGCAGAGTGGTGCGGTCCGTGCAAAATGATCGCCCCGAT
45 64 A I L V D F W A E W C G P C K M I A P I

TCTGGATGAAATCGCTGACGAATATCAGGGCAAACCTGACCGTTGCAAACTGAACATCGA
84 L D E I A D E Y Q G K L T V A K L N I D

50 TCAAAACCCTGGCACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTGCTGTT
104 Q N P G T A P K Y G I R G I P T L L L F

CAAAAACGGTGAAGTGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTGAAAGA
124 K N G E V A A T K V G A L S K G Q L K E

55

FLAG Lost XbaI
GAACCTGGCGGATTATAAAGATGACGATGACAAATAATAAGCTAGAGGTACC (trxn
stop)

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pMPX-83 MalE (1-370 del 354-364) MCS TrxA (2-109 del 103-107) fusion vector

SD Lost PstI +1

5 male (1-28)
2401 GAATTCAGGCGCTTTTCTAGACTGGTCGTAATGAAATTCAGGAGGTTCTGCATATGAAAAT
1 M K I

10 2461 AAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTC
4 K T G A R I L A L S A L T T M M F S A S

2521 GGCTCTCGCCAAAATCGAAGAAGGTAAACTGGTAATCTGGATTAACGGCGATAAAGGCTA
24 A L A K I E E G K L V I W I N G D K G Y

15 2581 TAACGGTCTCGCTGAAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAAGTCACCGT
44 N G L A E V G K K F E K D T G I K V T V

2641 TGAGCATCCGGATAAACTGGAAGAGAAATTCACACAGGTTGCGGCAACTGGCGATGGCCC
64 E H P D K L E E K F P Q V A A T G D G P

20 2701 TGACATTATCTTCTGGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGC
84 D I I F W A H D R F G G Y A Q S G L L A

2761 TGAAATCACCCCGACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGGGATGCCGT
25 104 E I T P D K A F Q D K L Y P F T W D A V

2821 ACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGATTTA
124 R Y N G K L I A Y P I A V E A L S L I Y

30 2881 TAACAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCGCTGGATAA
144 N K D L L P N P P K T W E E I P A L D K

2941 AGAACTGAAAGCGAAAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTACTTCAC
164 E L K A K G K S A L M F N L Q E P Y F T

35 3001 CTGGCCGCTGATTGCTGCTGACGGGGGTTATGCGTTCAAGTATGAAAACGGCAAGTACGA
184 W P L I A A D G G Y A F K Y E N G K Y D

3061 CATTAAAGACGTGGGCGTGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCCTGGTTGA
40 204 I K D V G V D N A G A K A G L T F L V D

3121 CCTGATTAAAAACAAACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCTGCCTT
224 L I K N K H M N A D T D Y S I A E A A F

45 3181 TAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATCGACAC
244 N K G E T A M T I N G P W A W S N I D T

3241 CAGCAAAGTGAATTATGGTGTAACGGTACTGCCGACCTTCAAGGGTCAACCATCCAAACC
264 S K V N Y G V T V L P T F K G Q P S K P

50 3301 GTTCGTTGGCGTGCTGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGCTGGCGAA
284 F V G V L S A G I N A A S P N K E L A K

3361 AGAGTTCCTCGAAAACATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAAGACAA
55 304 E F L E N Y L L T D E G L E A V N K D K

3421 ACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCACGTAT
324 P L G A V A L K S Y E E E L A K D P R I

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Factor Xa

3481 TGCCGCCACCATGGAAAACGCCAGTCCGCTTTCTGGTATGCCGTGCGTATCGAAGCCCG
344 A A T M E N A Q S A F W Y A V R I E A R

5 PstI Sall XbaI +2 trxA (2-109 del 103-107)
3541 CCTGCAGGCCTCGGTCGACGCCGAATCTAGAAGCGATAAAATTATTCACCTGACTGACGA
364 L Q A S V D A E S R S D K I I H L T D D

3601 CAGTTTTGACACGGATGTACTCAAAGCGGACGGGGCGATCCTCGTCGATTTCTGGGCAGA
10 384 S F D T D V L K A D G A I L V D F W A E

3661 GTGGTGCGGTCCGTGCAAAATGATCGCCCCGATTCTGGATGAAATCGCTGACGAATATCA
404 W C G P C K M I A P I L D E I A D E Y Q

15 3721 GGGCAAACCTGACCGTTGCAAACTGAACATCGATCAAAACCCTGGCACTGCGCCGAAATA
424 G K L T V A K L N I D Q N P G T A P K Y

3781 TGGCATCCGTGGTATCCCGACTCTGCTGCTGTTCAAAAACGGTGAAGTGGCGGCAACCAA
444 G I R G I P T L L L F K N G E V A A T K

20

FLAG

3841 AGTGGGTGCACTGTCTAAAGGTCAGTTGAAAGAGAACCTGGCGGATTATAAAGATGACGA
464 V G A L S K G Q L K E N L A D Y K D D D

25 3901 TGACAAATAATAAGCTAGAGG (transcriptional stop)
484 D K

pMPX-72::male(1-320 del 354-364)::FXa::PstI, SallI, XbaI::TrxA(1-109
del 103-107)::FLAG

30 Rhamnose inducible, clone into PstI, SallI, XbaI

Made by cutting TOPO NsiI-male (1-370 del 354-364)::FXa::PstI, SallI,
XbaI::FLAG-NheI insertion with NsiI & XbaI and cloning into pMPX-78
cut with PstI & XbaI.

35

SEQ ID NO.: 283

pMPX-82 Male (1-370 del 354-364) MCS TrxA (2-109 del 103-107) fusion vector

40

SD Lost PstI +1 male (1-370 del
352-362)

1621 CCATACCCGTTTTTTTGGGCTAGCAGGAGGCCCTGCATATGAAAATAAAACAGGTGCAC
1 M K I K T G A

45 1681 GCATCCTCGCATTATCCGCATTAAACGACGATGATGTTTTCCGCCTCGGCTCTCGCCAAAA
8 R I L A L S A L T T M M F S A S A L A K

1741 TCGAAGAAGGTAAACTGGTAATCTGGATTAAACGGCGATAAAGGCTATAACGGTCTCGCTG
50 28 I E E G K L V I W I N G D K G Y N G L A

1801 AAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAAGTCACCGTTGAGCATCCGGATA
48 E V G K K F E K D T G I K V T V E H P D

55 1861 AACTGGAAGAGAAATTCACACAGGTTGCGGCAACTGGCGATGGCCCTGACATTATCTTCT
68 K L E E K F P Q V A A T G D G P D I I F

1921 GGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGCTGAAATCACCCCGG
88 W A H D R F G G Y A Q S G L L A E I T P

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1981 ACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGGGATGCCGTACGTTACAACGGCA
108 D K A F Q D K L Y P F T W D A V R Y N G

5 2041 AGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGATTTATAACAAAGATCTGC
128 K L I A Y P I A V E A L S L I Y N K D L

10 2101 TGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGCGCTGGATAAAGAACTGAAAGCGA
148 L P N P P K T W E E I P A L D K E L K A

2161 AAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTACTTCACCTGGCCGCTGATTG
168 K G K S A L M F N L Q E P Y F T W P L I

15 2221 CTGCTGACGGGGGTTATGCGTTCAAGTATGAAAACGGCAAGTACGACATTAAAGACGTGG
188 A A D G G Y A F K Y E N G K Y D I K D V

2281 GCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCCTGGTTGACCTGATTAAAAACA
208 G V D N A G A K A G L T F L V D L I K N

20 2341 AACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAA
228 K H M N A D T D Y S I A E A A F N K G E

2401 CAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATCGACACCAGCAAAGTGAATT
248 T A M T I N G P W A W S N I D T S K V N

25 2461 ATGGTGTAAACGGTACTGCCGACCTTCAAGGGTCAACCATCCAAACCGTTCGTTGGCGTGC
268 Y G V T V L P T F K G Q P S K P F V G V

30 2521 TGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGCTGGCGAAAGAGTTCCTCGAAA
288 L S A G I N A A S P N K E L A K E F L E

2581 ACTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAAGACAAACCGCTGGGTGCCG
308 N Y L L T D E G L E A V N K D K P L G A

35 2641 TAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCACGTATTGCCGCCACCATGG
328 V A L K S Y E E E L A K D P R I A A T M

Factor Xa PstI
40 2701 AAAACGCCCAGTCCGCTTTCTGGTATGCCGTGCGTATCGAAGCCCCGCTGCAGGCCTCGG
348 E N A Q S A F W Y A V R I E A R L Q A S

SalI XbaI +2 trxA (2-109 del 103-107)
45 2761 TCGACGCCGAATCTAGAAGCGATAAAATTATTCACCTGACTGACGACAGTTTTGACACGG
368 V D A E S R S D K I I H L T D D S F D T

2821 ATGTA CTCAAAGCGGACGGGGCGATCCTCGTGGATTCTGGGCAGAGTGGTGCGGTCCGT
388 D V L K A D G A I L V D F W A E W C G P

50 2881 GCAAAATGATCGCCCCGATTCTGGATGAAATCGCTGACGAATATCAGGGCAAAC TGACCG
408 C K M I A P I L D E I A D E Y Q G K L T

2941 TTGCAAAACTGAACATCGATCAAAACCTTGGCACTGCGCCGAAATATGGCATCCGTGGTA
428 V A K L N I D Q N P G T A P K Y G I R G

55 3001 TCCCGACTCTGCTGCTGTTCAAAAACGGTGAAGTGGCGGCAACCAAAGTGGGTGCACTGT
448 I P T L L L F K N G E V A A T K V G A L

FLAG
60 3061 CTAAAGGTCAGTTGAAAGAGAACCTGGCGGATTATAAAGATGACGATGACAAATAATAAG
468 S K G Q L K E N L A D Y K D D D D K

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Lost XbaI

CTAGAGG (transcriptional stop)

- 5 pMPX-71::malE(1-370 del 354-364)::FXa::PstI, SalI, XbaI::TrxA(1-109 del 103-107)::FLAG
Arabinose inducible, clone into PstI, SalI, XbaI

- 10 Made by cutting TOPO NsiI-malE (1-370 del 354-364)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & XbaI and cloning into pMPX-79 cut with PstI & XbaI.

- 15 SEQ ID NO.: 284

pMPX-92 MalE (1-370 del 354-364) MCS TrxA (2-109 del 103-107) fusion vector

- 20 354-364) SD Lost PstI +1 malE (1-370 del
AGGAGGTTCTGCATATGAAAATAAAAAACAGGTGCAC
1 M K I K T G A
- 25 8 GCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTCGGCTCTCGCCAAAA
R I L A L S A L T T M M F S A S A L A K
- 28 TCGAAGAAGGTAACTGGTAATCTGGATTAACGGCGATAAAGGCTATAACGGTCTCGCTG
I E E G K L V I W I N G D K G Y N G L A
- 30 48 AAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAAGTCACCGTTGAGCATCCGGATA
E V G K K F E K D T G I K V T V E H P D
- 35 68 AACTGGAAGAGAAATTCACACAGGTTGCGGCAACTGGCGATGGCCCTGACATTATCTTCT
K L E E K F P Q V A A T G D G P D I I F
- 88 GGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGCTGAAATCACCCCGG
W A H D R F G G Y A Q S G L L A E I T P
- 40 108 ACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGGGATGCCGTACGTTACAACGGCA
D K A F Q D K L Y P F T W D A V R Y N G
- 128 AGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGATTATAACAAAGATCTGC
K L I A Y P I A V E A L S L I Y N K D L
- 45 148 TGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCGCTGGATAAAGAACTGAAAGCGA
L P N P P K T W E E I P A L D K E L K A
- 50 168 AAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTACTTCACCTGGCCGCTGATTG
K G K S A L M F N L Q E P Y F T W P L I
- 188 CTGCTGACGGGGTTATGCGTTCAAGTATGAAAACGGCAAGTACGACATTAAAGACGTGG
A A D G G Y A F K Y E N G K Y D I K D V
- 55 208 GCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCCTGTTGACCTGATTAAAAACA
G V D N A G A K A G L T F L V D L I K N
- 2341 AACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAA
228 K H M N A D T D Y S I A E A A F N K G E

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2401 CAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATCGACACCAGCAAAGTGAATT
248 T A M T I N G P W A W S N I D T S K V N

2461 ATGGTGTAACGGTACTGCCGACCTTCAAGGGTCAACCATCCAAACCGTTCGTTGGCGTGC
5 268 Y G V T V L P T F K G Q P S K P F V G V

2521 TGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGCTGGCGAAAGAGTTCCTCGAAA
288 L S A G I N A A S P N K E L A K E F L E

10 2581 ACTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAAGACAAACCGCTGGGTGCCG
308 N Y L L T D E G L E A V N K D K P L G A

2641 TAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCACGTATTGCCGCCACCATGG
328 V A L K S Y E E E L A K D P R I A A T M

15

2701 AAAACGCCCAGTCCGCTTTCTGGTATGCCGTGCGTATCGAAGCCCGCTGCAGGCCTCGG
348 E N A Q S A F W Y A V R I E A R L Q A S

20

SalI XbaI +2 trxA (2-109 del 103-107)
2761 TCGACGCCGAATCTAGAAGCGATAAAATTATTACCTGACTGACGACAGTTTTGACACGG
368 V D A E S R S D K I I H L T D D S F D T

2821 ATGTACTCAAAGCGGACGGGGCGATCCTCGTCGATTTCTGGGCAGAGTGGTGGGTCCGT
25 388 D V L K A D G A I L V D F W A E W C G P

2881 GCAAAATGATGCCCCGATTCTGGATGAAATCGCTGACGAATATCAGGGCAAACCTGACCG
408 C K M I A P I L D E I A D E Y Q G K L T

30 2941 TTGCAAACTGAACATCGATCAAAACCCTGGCACTGCGCCGAAATATGGCATCCGTGGTA
428 V A K L N I D Q N P G T A P K Y G I R G

3001 TCCCGACTCTGCTGCTGTTCAAAAACGGTGAAGTGGCGCAACCAAGTGGGTGCACTGT
448 I P T L L L F K N G E V A A T K V G A L

35

3061 CTAAAGGTCAGTTGAAAGAGAACCTGGCGGATTATAAAGATGACGATGACAAATAATAAG
468 S K G Q L K E N L A D Y K D D D D K

40

Lost XbaI
CTAGAGGTACC (transcriptional stop)

pMPX-84::male(1-370 del 354-364)::FXa::PstI, SalI, XbaI::TrxA(1-109
del 103-107)::FLAG
45 Temperature inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-male (1-370 del 354-364)::FXa::PstI, SalI,
XbaI::FLAG-NheI insertion with NsiI & XbaI and cloning into pMPX-90
cut with PstI & XbaI.
50

SEQ ID NO.: 285

55 pMPX-97 Male (1-370 del 354-364) MCS TrxA (2-109 del 103-107) fusion vector

SD Lost PstI +1 male (1-370 del
354-364)
AGGAGGTTCTGCATATGAAAATAAAAACAGGTGCAC

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1 M K I K T G A

5 GCATCCTCGCATTATCCGCATTAAACGACGATGATGTTTTCCGCCTCGGCTCTCGCCAAAA
8 R I L A L S A L T T M M F S A S A L A K

10 TCGAAGAAGGTAACTGGTAATCTGGATTAAACGGCGATAAAGGCTATAACGGTCTCGCTG
28 I E E G K L V I W I N G D K G Y N G L A

15 AAGTCGGTAAGAAATTCCGAGAAAGATACCGGAATTAAAGTCACCGTTGAGCATCCGGATA
48 E V G K K F E K D T G I K V T V E H P D

68 AACTGGAAGAGAAATTCCCACAGGTTGCGGCAACTGGCGATGGCCCTGACATTATCTTCT
K L E E K F P Q V A A T G D G P D I I F

20 GGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGCTGAAATCACCCCGG
88 W A H D R F G G Y A Q S G L L A E I T P

108 ACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGGGATGCCGTACGTTACAACGGCA
D K A F Q D K L Y P F T W D A V R Y N G

128 AGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGATTTATAACAAAGATCTGC
K L I A Y P I A V E A L S L I Y N K D L

25 TGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCGCTGGATAAAGAACTGAAAGCGA
148 L P N P P K T W E E I P A L D K E L K A

168 AAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTACTTCACCTGGCCGCTGATTG
K G K S A L M F N L Q E P Y F T W P L I

30 CTGCTGACGGGGTTATGCGTTCAAGTATGAAAACGGCAAGTACGACATTAAAGACGTGG
188 A A D G G Y A F K Y E N G K Y D I K D V

208 GCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCCTGGTTGACCTGATTAAAAACA
G V D N A G A K A G L T F L V D L I K N

35 AACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAA
2341 K H M N A D T D Y S I A E A A F N K G E

2401 CAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATCGACACCAGCAAAGTGAATT
248 T A M T I N G P W A W S N I D T S K V N

2461 ATGGTGTAACGGTACTGCCGACCTTCAAGGGTCAACCATCCAAACCGTTGTTGGCGTGC
268 Y G V T V L P T F K G Q P S K P F V G V

45 TGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGCTGGCGAAAGAGTTCTCTCGAAA
2521 L S A G I N A A S P N K E L A K E F L E

2581 ACTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAAGACAAACCGCTGGGTGCCG
308 N Y L L T D E G L E A V N K D K P L G A

50 TAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCACGTATTGCCGCCACCATGG
2641 V A L K S Y E E E L A K D P R I A A T M

328

55 2701 AAAACGCCCAGTCCGCTTTCTGGTATGCCGTGCGTATCGAAGCCCGCTGCAGGCCTCGG
348 E N A Q S A F W Y A V R I E A R L Q A S

Factor Xa PstI

2761 TCGACGCCGAATCTAGAAAGCGATAAAATTATTCACCTGACTGACGACAGTTTTGACACGG
368 V D A E S R S D K I I H L T D D S F D T

60

Sall XbaI +2 trxA (2-109 del 103-107)

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2821 ATGTACTCAAAGCGGACGGGGCGATCCTCGTCGATTTCTGGGCAGAGTGGTGCGGTCCGT
388 D V L K A D G A I L V D F W A E W C G P

5 2881 GCAAAATGATCGCCCCGATTCTGGATGAAATCGCTGACGAATATCAGGGCAAACCTGACCG
408 C K M I A P I L D E I A D E Y Q G K L T

2941 TTGCAAACTGAACATCGATCAAAACCCTGGCACTGCGCCGAAATATGGCATCCGTGGTA
428 V A K L N I D Q N P G T A P K Y G I R G

10 3001 TCCCGACTCTGCTGCTGTTCAAAAACGGTGAAGTGGCGGCAACCAAAGTGGGTGCACTGT
448 I P T L L L F K N G E V A A T K V G A L

15 3061 FLAG
468 CTAAAGGTCAGTTGAAAGAGAACCTGGCGGATTATAAAGATGACGATGACAAATAATAAG
S K G Q L K E N L A D Y K D D D D K

Lost XbaI
CTAGAGGTACC (transcriptional stop)

20 pMPX-86::malE(1-370 del 354-364)::FXa::PstI, SalI, XbaI::TrxA(1-109 del
103-107)::FLAG

Temperature inducible, clone into PstI, SalI, XbaI

25 Made by cutting TOPO NsiI-malE (1-370 del 354-364)::FXa::PstI, SalI,
XbaI::FLAG-NheI insertion with NsiI & XbaI and cloning into pMPX-95
cut with PstI & XbaI.

30